



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 154940

TO: Bao-Qun Li
Location: rem/3d24/3c18
Art Unit: 1648
Monday, June 06, 2005

Case Serial Number: 10/649480

From: Alex Waclawiw
Location: Biotech-Chem Library
CM1-6A02
Phone: 308-4491

Alexandra.waclawiw@uspto.gov

Search Notes

BEST AVAILABLE COPY

This Page Blank (uspto)

STIC-Biotech/ChemLib

1574940

From: Li, Bao-Qun
Sent: Tuesday, May 31, 2005 1:52 PM
To: STIC-Biotech/ChemLib
Subject: 10,649,480

Please do the sequence homology and interference search for SEQ ID NO: 7, and 2.

Bao Qun Li M.D
TC 1600
Art Unit 1648
Tel. 517-272-0904
REM, 3C18
Rm. 3D24

RECEIVED
MAY 31 2005
STIC

STAFF USE ONLY
Point of Contact:
Alexandra Wacławiw
Technical Info. Specialist
CM1-6A02 Tel. 308-4491

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: 6-6-05
Date Completed: 6-6-05
Searcher Prep/Rev. Time: _____
Online Time: 14

Type of Search

NA#: _____ AA#: 2
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

BEST AVAILABLE COPY

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model
Run on: June 6, 2005, 07:37:37 ; Search time 109.561 Seconds
(without alignments)
497.744 Million cell updates/sec

Title: US-10-649-480A-7
Perfect score: 762
Sequence: 1 MFNLPNGYKPKLLYCNSG.....PRTHYGQKAILFLPLPVSSD 141

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	762	100.0	141	2 AAR10527	Aar10527 Human aci
2	762	100.0	141	5 AAU76945	Aau76945 Human aci
3	762	100.0	141	5 AAO19992	Aao19992 Protein o
4	762	100.0	141	8 ADO5206	Ado5206 Human aci
5	762	100.0	151	2 AAR05789	Aar05789 Human aFG
6	757	99.3	140	1 AAP70995	Aap70995 Sequence
7	757	99.3	140	1 AAP90068	Aap90068 Human aci
8	757	99.3	140	2 AAR25914	Aar25914 Human aci
9	757	99.3	140	2 AAR34497	Aar34497 Human aci
10	757	99.3	140	2 AAR74647	Aar74647 Human aci
11	757	99.3	140	2 AAW04806	Aaw04806 Human aci
12	757	99.3	154	2 AAW04805	Aaw04805 Human bet
13	757	99.3	154	2 AAW06816	Aaw06816 Human end
14	757	99.3	154	2 AAW75414	Aaw75414 Human bet
15	757	99.3	154	2 AAW92283	Aaw92283 Human bet
16	757	99.3	154	6 ABR63868	AbR63868 Thrombin
17	757	99.3	154	8 ADO55207	Ado55207 Processed
18	757	99.3	155	1 AAP70482	Aap70482 Sequence
19	757	99.3	155	1 AAP94037	Aap94037 Human aci
20	757	99.3	155	2 AAR70812	Aar70812 FGF-1. 3/
21	757	99.3	155	2 AAR80776	Aar80776 Fibroblas
22	757	99.3	155	2 AAW75711	Aaw75711 Fibroblas
23	757	99.3	155	2 AAW75415	Aaw75415 Human end
24	757	99.3	155	2 AAW53022	Aaw53022 Fibroblas
25	757	99.3	155	2 AAW92291	Aaw92291 Human end

26	757	99.3	155	2 AAY08584	Aay08584 Human FGF
27	757	99.3	155	3 AAY32333	Aay32333 Human fib
28	757	99.3	155	3 AAY90410	Aay90410 FGF-1, SE
29	757	99.3	155	3 AAB10297	Aab10297 Fibroblas
30	757	99.3	155	4 AAB50705	Aab50705 Human fib
31	757	99.3	155	4 AAB61661	Aab61661 FGF1 prot
32	757	99.3	155	4 AAB50298	Aab50298 Human fib
33	757	99.3	155	4 AAB50273	Aab50273 Human aci
34	757	99.3	155	4 AAB5812	Aab5812 Human fib
35	757	99.3	155	5 AAU76943	Aau76943 Human aci
36	757	99.3	155	5 AAO19990	Aao19990 Protein o
37	757	99.3	155	5 AAO19994	Aao19994 Protein o
38	757	99.3	155	5 ABB99120	Abb99120 Human fib
39	757	99.3	155	6 ABP54277	Abp54277 Human fib
40	757	99.3	155	6 ADA95452	Ada95452 Fibroblas
41	757	99.3	155	7 ADC34576	Adc34576 Human fib
42	757	99.3	155	7 ABR56165	AbR56165 Human Fib
43	757	99.3	155	7 ADD66125	Add66125 Fibroblas
44	757	99.3	155	7 ADH92000	Adh92000 Fibroblas
45	757	99.3	155	8 ADO55201	Ado55201 Human aci

ALIGNMENTS

RESULT 1
AAR10527
ID// AAR10527 standard; protein; 141 AA.
XX
AC AAR10527;
XX
DT 25-MAR-2003 (revised)
DT 15-APR-1991 (first entry)
XX
DE Human acidic fibroblast growth factor gene.
XX
KW aFGF; antibody; antigen; cancer; ss.
XX
OS Homo sapiens.

PH Key Location/Qualifiers
FT Region 2..12
FT Region /label= A
FT Region 56..67
FT Region /label= B
FT Region 104..114
FT Region /label= C
FT Region 132..141
FT Region /label= D

XX JP02306996-A.

XX 20-DEC-1990.

PF 03-JUL-1989; 89JP-00172542.

PR 04-JUL-1988; 88JP-00166275.

XX (TAKE) TAKEDA CHEM IND LTD.

DR WPI; 1991-040150/06.

DR N-PSDB; AAQ10399.

XX Anti-acid antibody, for cancer diagnosis, etc. - is obt'd. by using complex of partial peptide(s) of acid fibroblast growth factor and protein as antigen.

PS Disclosure; Fig 1; 19pp; Japanese.

XX The was deduced from a gene used to produce recombinant aFGF. Peptides derived from the protein, esp. from A-D can be used to as antigens to produce anti-aFGF antibodies. The peptides must comprise 8-10 continuous AAs from A or B (claims 5 and 6 resp.), 7-10 continuous AAs from C (claim

7), or 8-9 continuous AAs from D (claim 8). The Abs can be used for immunochemically measuring aFGF, and for purifying aFGF. They are useful as reagents in the diagnosis of various cancers or diseases of the CNS. Purified aFGF has wound healing and nerve cell proliferating properties. (Updated on 25-MAR-2003 to correct PA field.)

CC CC CC CC CC CC CC
XX XX XX XX XX XX
SQ Sequence 141 AA;
Query Match 100.0%; Score 762; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 1.7e-78;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFNLPPGNYKKPKLLYCSNGGHFLRLIPDGTGVDGTRDRSDQHILQLSAESVGEVYIKST 60
Db 1 MFNLPPGNYKKPKLLYCSNGGHFLRLIPDGTGVDGTRDRSDQHILQLSAESVGEVYIKST 60
Qy 61 ETGOYLANDTDGLLYGSGTNPNECLFLERLEENHYNTYISKHAEKNWVGLKXGSCKR 120
Db 61 ETGOYLANDTDGLLYGSGTNPNECLFLERLEENHYNTYISKHAEKNWVGLKXGSCKR 120
Qy 121 GPRTHYGOKAILFLPLPVSSD 141
Db 121 GPRTHYGOKAILFLPLPVSSD 141

RESULT 2
AAU76945
ID AAU76945 standard; protein; 141 AA.
XX AAU76945;
XX
XX
DT 05-JUN-2002 (first entry)
XX
DE Human acidic FGF protein HAEGF140.
XX
KW HAEGF140; acidic fibroblast growth factor; cell proliferation;
KW differentiation; tumorigenesis; metastasis; angiogenesis; chromosome 5;
KW human.
OS Homo sapiens.
OS Synthetic.
XX
FN WO200214471-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US025537.
XX
PR 15-AUG-2000; 2000US-0225406P.
XX
PA (PHAG-) PHAGE BIOTECHNOLOGY CORP.
XX
PI Stegmann TJ, Kordyum VA, Chernykh SI, Slavchenko IV, Vozianov OF;
XX
XX WPI; 2002-257598/30.
DR N-PSDB; ABK10595.
XX
XX Producing a biologically active human acidic fibroblast growth factor
PT (haFGF) protein for use in promoting angiogenesis, involves employing an
PT E. coli transformed with a plasmid having an haFGF gene operably linked
PT to a promoter.
XX
XX Example 3; Fig 8; 41pp; English.
XX
XX This invention relates to a novel method for producing a biologically
CC active human acidic fibroblast growth factor (haFGF) protein. Fibroblast
CC growth factors are potent regulators of cell proliferation,
CC differentiation and normal development and they have been shown to play a
CC role in tumorigenesis and metastasis. Acidic fibroblast growth factor
CC has been shown to be potent inducers of angiogenesis. The gene for acidic
CC fibroblast growth factor is located on human chromosome 5. The method of
CC the invention comprises employing a plasmid having at least one copy of
CC gene, which encodes a biologically active haFGF protein operably linked

to a promoter, to transform Escherichia coli. The method is useful for producing recombinant or biologically active haFGF protein, which is useful in promoting angiogenesis. The present sequence represents the human acidic fibroblast growth factor 140 protein (haFGF140) used in the method of the invention

CC CC CC CC CC CC CC
XX XX XX XX XX XX
SQ Sequence 141 AA;
Query Match 100.0%; Score 762; DB 5; Length 141;
Best Local Similarity 100.0%; Pred. No. 1.7e-78;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFNLPPGNYKKPKLLYCSNGGHFLRLIPDGTGVDGTRDRSDQHILQLSAESVGEVYIKST 60
Db 1 MFNLPPGNYKKPKLLYCSNGGHFLRLIPDGTGVDGTRDRSDQHILQLSAESVGEVYIKST 60
Qy 61 ETGOYLANDTDGLLYGSGTNPNECLFLERLEENHYNTYISKHAEKNWVGLKXGSCKR 120
Db 61 ETGOYLANDTDGLLYGSGTNPNECLFLERLEENHYNTYISKHAEKNWVGLKXGSCKR 120
Qy 121 GPRTHYGOKAILFLPLPVSSD 141
Db 121 GPRTHYGOKAILFLPLPVSSD 141

RESULT 3
AAO19992
ID AAO19992 standard; protein; 141 AA.
XX AAO19992;
XX
XX 24-MAY-2002 (first entry)
XX
XX Protein of chemically synthesised human A FGF (140AA).
XX
KW Human acidic fibroblast growth factor; phage T7 polymerase promoter;
KW lysis; phage dependent superproduction; A FGF.
XX
XX Homo sapiens.
XX WO200214468-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US025477.
XX
PR 15-AUG-2000; 2000US-0225437P.
XX
PA (PHAG-) PHAGE BIOTECHNOLOGY CORP.
XX
XX Kordyum VA, Chernykh SI, Slavchenko IV, Vozianov OF;
PI
XX WPI; 2002-269184/31.
DR N-PSDB; AAK98920.
XX
XX Bacteriophage-dependent method for producing biologically active proteins
PT or peptides, involves employing an Escherichia coli transformed with a
PT plasmid containing the targeted gene(s) operably linked to a promoter.
XX
XX Example 3; Fig 8; 44pp; English.
XX
XX The invention relates to a method for enhancing the production of a
CC biologically active protein comprising infecting a strain of Escherichia
CC coli, which has been transformed with a plasmid having at least one copy
CC of an expressible gene, such as a human acidic fibroblast growth factor.
CC The expressible gene encodes a biologically active protein operably
CC linked to a phage T7 polymerase promoter, with a bacteriophage capable of
CC mediating delayed lysis. The method is useful for the phage dependent
CC superproduction of biologically active protein and peptides. The method
CC is particularly useful for enhancing the production of heterologous
CC proteins in bacterial host cells. This sequence represents the protein of
CC a chemically synthesised human acidic fibroblast growth factor - human A
CC FGF (140AA) of the invention

XX Sequence 141 AA;
SQ Query Match 100.0%; Score 762; DB 5; Length 141;
Best Local Similarity 100.0%; Pred. No. 1.7e-78;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFNLPPGNYKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHIQLQLSAESVGEVIYKST 60
Db 1 MFNLPPGNYKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHIQLQLSAESVGEVIYKST 60

Qy 61 ETGOYLAMDTGLLYGSQTPNEECFLERLEENHYNTYISKHAEKNWFWGLKNGSCKR 120
Db 61 ETGOYLAMDTGLLYGSQTPNEECFLERLEENHYNTYISKHAEKNWFWGLKNGSCKR 120

Qy 121 GPRTHYGOKAILFLPLPVSSD 141
Db 121 GPRTHYGOKAILFLPLPVSSD 141

RESULT 4
AD055206
ID AD055206 standard; protein; 141 AA.
AC AD055206;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human acidic fibroblast growth factor (hAFGF) seqid 7.
XX
KW neangiogenesis stimulator; cardiant; vasotropic; revascularisation;
KW ischaemic region; fibroblast growth factor-1; FGF-1; neoangiogenesis;
KW acidic FGF; aFGF; bacteriophage lambda; coronary artery disease;
KW myocardial perfusion; revascularisation therapy; ischaemic myocardium;
KW human.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2004115769-A1.
XX
PD 17-JUN-2004.
XX
PF 27-AUG-2003; 2003US-00649480.
XX
PR 24-JUL-1998; 98US-0093962P.
PR 22-JUL-1999; 99US-00358780.
PR 15-AUG-2000; 2000US-0225406P.
PR 15-AUG-2001; 2001US-00929945.
XX
PA (STEG/) STEGMANN T J.
PA (KORD/) KORDYUM V A.
PA (SLAV/) SLAVCHENKO I Y.
PA (CHER/) CHERNYKH S I.
PA (VOZI/) VOZIANOV O F.
XX
XX Stegmann TJ, Kordyum VA, Slavchenko IY, Chernykh SI, Vozianov OF;
PI WPI; 2004-449397/42.
DR N-PSDB; AD055205.
XX
XX Revascularizing an ischemic region, for treating coronary artery disease,
PT comprises preparing and injecting a composition comprising a recombinant
PT human fibroblast growth factor-1 into the ischemic region to induce local
PT neoangiogenesis.
XX
XX Claim 12; SEQ ID NO 7; 42pp; English.
PS
XX
XX The invention describes revascularising an ischaemic region comprising
CC preparing a pharmaceutical composition comprising a recombinant
CC fibroblast growth factor-1 (FGF-1) and injecting an amount of the
CC pharmaceutical composition into the ischaemic region, the amount being
CC sufficient to induce local neoangiogenesis. The FGF-1 is prepared by

CC transforming an Escherichia coli host cell with a plasmid comprising an
CC expressible gene encoding a biologically active human acidic FGF protein,
CC operably linked to a promoter; infecting the transformed bacterial host
CC cell with a bacteriophage λ gr; which mediates delayed lysis; and
CC culturing the E. coli host cell under a culture condition that induces
CC lytic growth of the cell without lysis until a desired level of
CC production of the protein is reached, where the protein is produced as a
CC soluble, biologically-active human acidic FGF protein. Also described is
CC a method of treating coronary artery disease in a patient, comprising
CC preparing a pharmaceutical composition comprising a recombinant FGF-1;
CC injecting an amount of the pharmaceutical composition into at least one
CC site in a heart wall, the amount being sufficient to improve myocardial
CC perfusion; and injecting a composition comprising a physiological glue to
CC a surface of the heart at the site(s) where the pharmaceutical
CC composition was injected. The methods are useful for treating coronary
CC heart disease by revascularisation therapy or for inducing local
CC neoangiogenesis in ischaemic myocardium. This is the amino acid sequence
CC of human acidic fibroblast growth factor (hAFGF), the DNA encoding which
CC has been modified by substitution of naturally occurring codons with
CC codons found in highly expressed E.coli proteins.
XX
SQ Sequence 141 AA;

Query Match 100.0%; Score 762; DB 8; Length 141;
Best Local Similarity 100.0%; Pred. No. 1.7e-78;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFNLPPGNYKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHIQLQLSAESVGEVIYKST 60
Db 1 MFNLPPGNYKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHIQLQLSAESVGEVIYKST 60

Qy 61 ETGOYLAMDTGLLYGSQTPNEECFLERLEENHYNTYISKHAEKNWFWGLKNGSCKR 120
Db 61 ETGOYLAMDTGLLYGSQTPNEECFLERLEENHYNTYISKHAEKNWFWGLKNGSCKR 120

Qy 121 GPRTHYGOKAILFLPLPVSSD 141
Db 121 GPRTHYGOKAILFLPLPVSSD 141

RESULT 5
AAR05789
ID AAR05789 standard; protein; 151 AA.
XX
XX AAR05789;
XX
DT 22-AUG-1990 (first entry)
XX
DE Human aFGF encoded by synthetic gene.
XX
KW Acidic fibroblast growth factor; aFGF; thrombogenesis; atherosclerosis;
KW tumors.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 146..147
FT /note= "sites corresp. to two stop codons of the DNA
FT sequence"
XX
XX GB2223496-A.
XX
PD 11-APR-1990.
XX
PF 08-AUG-1988; 88GB-00018775.
XX
PR 08-AUG-1988; 88GB-00018775.
XX
PA (BRBI-) BRIT BIO-TECH LTD.
XX
XX Davies JA, Johnson ID;
XX
XX WPI; 1990-109882/15.
DR

DR N-PSDB; AAQ03873.
XX
XX Gene encoding human acidic fibroblast growth factor - incorporates useful
PT restriction sites at frequent intervals to facilitate cassette
PT mutagenesis of specified regions.
XX
XX Claim 2; Fig 3a; 12pp; English.
XX
XX The synthetic aFGF gene incorporates useful restriction sites at frequent
CC intervals to facilitate the cassette mutagenesis of selected regions.
CC Also included are flanking sites to simplify the incorporation of the
CC gene into any expression system. The aFGF mol. acts in a cascade effect
CC to control endothelial cell activity either co-ordinately through
CC synergistic effects or via independent routes. The regulation of
CC endothelial cells is essential for the protection of arteries, veins and
CC capillaries from the effect of thrombogenesis. Their stimulation and
CC control by these factors is also thought to be important in the
CC development of tumours and atherosclerosis
XX
XX Sequence 151 AA;
Query Match 100.0%; Score 762; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.8e-78;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFNLPNGNYKKPKLLYCSNGGHFLRILPDGTVGTRDRSDQHIQLQLSAESVGEVIKST 60
Db 5 MFNLPNGNYKKPKLLYCSNGGHFLRILPDGTVGTRDRSDQHIQLQLSAESVGEVIKST 64
Qy 61 ETGQYLAMDTGLLYGSGTNPNEECFLERLEENHYNTYISKHAEKNWFGVLKKGSKCR 120
Db 65 ETGQYLAMDTGLLYGSGTNPNEECFLERLEENHYNTYISKHAEKNWFGVLKKGSKCR 124
Qy 121 GPRTHYGOKAILFLPLPVSSD 141
Db 125 GPRTHYGOKAILFLPLPVSSD 145
RESULT 6
AAP70995
ID AAP70995 standard; protein; 140 AA.
XX
XX AAP70995;
XX
XX 13-JUN-1991 (first entry)
XX
XX Sequence of human proteinaceous factor (PFI) with mitogenic activity.
XX
XX Cell growth promoter; mitogen; vascularisation; wound healing.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Misc-difference 140
FT /label= Asp-OH
XX
XX **EP241136-A.**
XX
XX 14-OCT-1987.
XX
XX 06-MAR-1987; 87EP-00301969.
XX
XX 07-MAR-1986; 86US-00838096.
XX
XX (HARD) HARVARD COLLEGE.
XX
XX Lobb RR, Harper JW, Strydom DJ;
XX
XX WPI; 1987-285995/41.
XX
XX Mitogenic polypeptide isolated from human brain tissue - useful for
PT increasing vascular effect in e.g. wound healing, or generating
PT endothelial cell linings for vascular prostheses, etc.

XX Claim 3; Page 1; 31pp; English.
XX
XX The PF of the invention was obt'd. from human brain tissue. It has a mol.
CC wt. of 15,200-16,500 (pref. 15,616-16,056) and has a high affinity for
CC heparin. PFI and fragments are useful for promoting the growth of
CC mesoderm-derived cells or neuroectoderm-derived cells and generating
CC endothelial cell linings for vascular prostheses (all claimed).The
CC polypeptides are useful for increasing vascularisation
XX
XX Sequence 140 AA;
Query Match 99.3%; Score 757; DB 1; Length 140;
Best Local Similarity 100.0%; Pred. No. 6.1e-78;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 FNLPPGNYKKPKLLYCSNGGHFLRILPDGTVGTRDRSDQHIQLQLSAESVGEVIKSTE 61
Db 1 FNLPPGNYKKPKLLYCSNGGHFLRILPDGTVGTRDRSDQHIQLQLSAESVGEVIKSTE 60
Qy 62 TGQYLAMDTGLLYGSGTNPNEECFLERLEENHYNTYISKHAEKNWFGVLKKGSKCRG 121
Db 61 TGQYLAMDTGLLYGSGTNPNEECFLERLEENHYNTYISKHAEKNWFGVLKKGSKCRG 120
Qy 122 PRTHYGOKAILFLPLPVSSD 141
Db 121 PRTHYGOKAILFLPLPVSSD 140
RESULT 7
AAP90068
ID AAP90068 standard; protein; 140 AA.
XX
XX AAP90068;
XX
XX 25-MAR-2003 (revised)
DT 01-NOV-1989 (first entry)
XX
XX Human acid fibroblast growth factor.
XX
XX Human acidic fibroblast growth factor; mutant.
XX
XX Homo sapiens.
XX
XX **EP319052-A.**
XX
XX 07-JUN-1989.
XX
XX 14-OCT-1988; 88EP-00202306.
XX
XX 22-OCT-1987; 87US-00112600.
XX
XX 16-SEP-1988; 88US-00244431.
XX
XX (MERI) MERCK & CO INC.
XX
XX Thomas KA, Linemeyer DL;
XX
XX WPI; 1989-167092/23.
XX
XX Mutant acidic fibroblast growth factor - used for promoting repair of
PT soft tissue, musculo-skeletal tissue or vascular or nerve tissue and
PT plasminogen activator prodn.
XX
XX Disclosure; Page 4; 36pp; English.
XX
XX Amino acid sequence of human acidic fibroblast growth factor (aFGF). The
CC patent claims mutant forms which have increased biological activity
CC with(out) heparin, and promote cell growth. (Updated on 25-MAR-2003 to
CC correct PD field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated
CC on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 140 AA;

Query Match 99.3%; Score 757; DB 1; Length 140;
Best Local Similarity 100.0%; Pred. No. 6.1e-78;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FNLPPGNYKKPKLLYCSNGGHFLRILPDGTVDGTRDSQHIQLQLSAESVGEVYIKSTE 61
DB 1 FNLPPGNYKKPKLLYCSNGGHFLRILPDGTVDGTRDSQHIQLQLSAESVGEVYIKSTE 60

QY 62 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAEKNWVFLKKGSCCKRG 121
DB 61 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAEKNWVFLKKGSCCKRG 120

QY 122 PRTHYGOKAILFLPLPVSSD 141
DB 121 PRTHYGOKAILFLPLPVSSD 140

RESULT 8
AAR25914
ID AAR25914 standard; peptide; 140 AA.
XX
AC AAR25914;
XX
DT 25-MAR-2003 (revised)
DT 26-JAN-1993 (first entry)
XX
DE Human acidic fibroblast growth factor.
XX
KW viral infections; viruses; FGF; herpes simplex virus; HSV-1; HSV-2;
KW herpes varicella; herpes zoster; cytomegalovirus; influenza;
KW human respiratory syncytial virus; Semliki Forest virus; HIV;
KW human immunodeficiency virus; Moloney Sarcoma virus.
XX
OS Homo sapiens.
XX
PN EP497341-A2-
XX
PD 05-AUG-1992.
XX
XX 30-JAN-1992; 92EP-00101541.
XX
PF 31-JAN-1991; 91GB-00002145.
PR 09-JAN-1992; 92GB-00000410.
XX
XX (FARM) FARMITALIA ERBA SRL CARLO.
XX
XX Ungheri D, Garofano L, Battistini C, Carminati P, Mazue G;
XX
XX WPI; 1992-260792/32.
XX
XX Synergistic antiviral composition contains BFGF and sulphated
PT polysaccharide - for treating viral infections e.g. HSV-1 and -2,
PT cytomegalovirus, HIV, influenza virus etc.
XX
XX Disclosure; Page 4; 20pp; English.
XX
XX This sequence represents acidic fibroblast growth factor (aFGF). aFGF, or
CC its fragments may be used in a synergistic compen. with an antivirally
CC active sulphated polysaccharide, and one or more excipients. The compen.
CC may be used to control herpes simplex virus (HSV-1 or -2) herpes
CC varicella/zoster; cytomegalovirus; influenza; human respiratory syncytial
CC virus; Semliki Forest virus; HIV or Moloney Sarcoma virus. The
CC combination of aFGF with sulphated polysaccharide is found to have a
CC greater antiviral activity than expected for an additive effect. See also
CC AAR25913-5. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 140 AA;
XX

Query Match 99.3%; Score 757; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 6.1e-78;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FNLPPGNYKKPKLLYCSNGGHFLRILPDGTVDGTRDSQHIQLQLSAESVGEVYIKSTE 61
DB 1 FNLPPGNYKKPKLLYCSNGGHFLRILPDGTVDGTRDSQHIQLQLSAESVGEVYIKSTE 60

QY 62 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAEKNWVFLKKGSCCKRG 121
DB 61 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAEKNWVFLKKGSCCKRG 120

QY 122 PRTHYGOKAILFLPLPVSSD 141
DB 121 PRTHYGOKAILFLPLPVSSD 140

RESULT 9
AAR34497
ID AAR34497 standard; protein; 140 AA.
XX
AC AAR34497;
XX
DT 06-AUG-1993 (first entry)
XX
DE Human acidic Fibroblast Growth Factor.
XX
KW aFGF; mutein; glycosylation site; glycoprotein.
XX
OS Homo sapiens.
XX
PN JP05076356-A.
XX
XX 30-MAR-1993.
XX
PF 30-MAY-1991; 91JP-00127435.
XX
PR 31-MAY-1990; 90JP-00143388.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX WPI; 1993-139564/17.
XX
XX FGF mutein prepn. useful for therapy of burn or thrombosis - by
PT transformation of lymphocyte-contained animal cell by vector contg. DNA
PT encoding FGF mutein.
XX
XX Disclosure; Page 3; 23pp; Japanese.
XX
XX The invention covers muteins of FGF (esp. bFGF) which contain at least
CC one glycosylation site. The muteins can be used to treat burns and
CC thrombosis
XX
XX Sequence 140 AA;
XX

Query Match 99.3%; Score 757; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 6.1e-78;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FNLPPGNYKKPKLLYCSNGGHFLRILPDGTVDGTRDSQHIQLQLSAESVGEVYIKSTE 61
DB 1 FNLPPGNYKKPKLLYCSNGGHFLRILPDGTVDGTRDSQHIQLQLSAESVGEVYIKSTE 60

QY 62 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAEKNWVFLKKGSCCKRG 121
DB 61 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAEKNWVFLKKGSCCKRG 120

QY 122 PRTHYGOKAILFLPLPVSSD 141
DB 121 PRTHYGOKAILFLPLPVSSD 140

RESULT 10
AAR74647
ID AAR74647 standard; protein; 140 AA.
XX
AC AAR74647;
XX

DT 25-MAR-2003 (revised)
DT 25-SEP-1995 (first entry)
XX Human recombinant aFGF.
XX Acidic fibroblast growth factor; aFGF; vulnery; angiogenesis; mitogen.
XX Homo sapiens.
XX US5401832-A.
XX 28-MAR-1995.
XX 25-SEP-1992; 92US-00951365.
XX 24-DEC-1984; 84US-00685923.
XX 12-SEP-1985; 85US-00774359.
XX 30-MAY-1986; 86US-00868473.
XX 11-JUL-1986; 86US-00884460.
XX 04-JUN-1987; 87US-00054991.
XX 04-MAY-1988; 88US-00190293.
XX 08-FEB-1991; 91US-00654397.
XX 25-SEP-1991; 91US-00765472.
XX (MERI) MERCK & CO INC.
XX Linemeyer DL, Thomas KA, Kelly LJ, Gimenez-Gallego G;
XX WPI; 1995-138983/18.
XX New recombinant human acidic fibroblast growth factor - used to promote
XX cell growth, to promote wound healing, for vascular grafts and blood
XX vessel repair.
XX Claim 2; Col 30; 25pp; English.
XX Oligonucleotides were synthesized on the basis of the amino acid sequence
XX of bovine acidic fibroblast growth factor (aFGF) and used to produce a
XX synthetic gene (given in AAQ88233) incorporating codons preferred by E.
XX coli or mammalian cells, unique cloning sites, etc. This synthetic gene
XX was mutagenized to obtain a gene encoding a human recombinant aFGF
XX (AAR74647) having activity equivalent to the native protein. (Updated on
XX 25-MAR-2003 to correct PF field.)
SQ Sequence 140 AA;
Query Match 99.3%; Score 757; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 6.1e-78;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 FNLPPGNYKKPKLLYCSNGGHFLRILPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
Db 1 FNLPPGNYKKPKLLYCSNGGHFLRILPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 60
Qy 62 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAEKNWVGLKKGCKRG 121
Db 61 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAEKNWVGLKKGCKRG 120
Qy 122 PRTHYGQKAILFLPLPVSSD 141
Db 121 PRTHYGQKAILFLPLPVSSD 140
RESULT 11
AAW04806
ID AAW04806 standard; protein; 140 AA.
XX AC AAW04806;
XX 25-MAR-2003 (revised)
DT 29-DEC-1996 (first entry)
XX Human acidic fibroblast growth factor.

XX Endothelial cell growth factor; ECGF; blood vessel; regeneration;
KW heparin-Sepharose affinity chromatography; probe; oligonucleotide; FGF;
KW fibroblast growth factor; ss.
XX Homo sapiens.
XX US552528-A.
XX 03-SEP-1996.
XX 03-NOV-1994; 94US-00334884.
XX 03-MAR-1986; 86US-00835594.
XX 18-DEC-1987; 87US-00134499.
XX 29-APR-1991; 91US-00693079.
XX 27-NOV-1991; 91US-00799859.
XX (RHON) RHONE POULENC RORER PHARM INC.
XX Maciag T, Burgess W;
XX WPI; 1996-412132/41.
XX N-PSDB; AAT37503.
XX Isolated, purified, biologically active bovine beta endothelial cell
XX growth factor - useful to regenerate or treat damaged blood vessels.
XX Disclosure; Fig 8; 28pp; English.
XX Bovine beta-endothelial cell growth factor (beta-ECGF; AAW03999) having a
XX mol.wt. of 20 kD can be purified at least 16300 fold from bovine brain
XX using heparin-Sepharose affinity chromatography. ECGF is useful for,
XX among other purposes, diagnostic applications and has potential in the
XX treatment of damaged blood vessels or other endothelial cell-lined
XX structures. Human ECGF (AAT37503) or fragments may be obtained using
XX oligonucleotides (AAT37504 and AAT37508 to AAT37509) whose design is
XX based on the sequence of bovine alpha- and beta-ECGF. (Updated on 25-MAR-
XX 2003 to correct PF field.)
SQ Sequence 140 AA;
Query Match 99.3%; Score 757; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 6.1e-78;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 FNLPPGNYKKPKLLYCSNGGHFLRILPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
Db 1 FNLPPGNYKKPKLLYCSNGGHFLRILPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 60
Qy 62 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAEKNWVGLKKGCKRG 121
Db 61 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAEKNWVGLKKGCKRG 120
Qy 122 PRTHYGQKAILFLPLPVSSD 141
Db 121 PRTHYGQKAILFLPLPVSSD 140
RESULT 12
AAW04805
ID AAW04805 standard; protein; 154 AA.
XX AC AAW04805;
XX 25-MAR-2003 (revised)
DT 29-DEC-1996 (first entry)
XX Human beta-endothelial cell growth factor.
XX Endothelial cell growth factor; ECGF; blood vessel; regeneration;
KW heparin-Sepharose affinity chromatography; probe; oligonucleotide; FGF;
KW fibroblast growth factor.

```

XX Homo sapiens.
XX US5552528-A.
XX 03-SEP-1996.
XX 03-NOV-1994; 94US-00334884.
XX 03-MAR-1986; 86US-00835594.
XX 18-DEC-1987; 87US-00134499.
XX 29-APR-1991; 91US-00693079.
XX 27-NOV-1991; 91US-00799859.
XX (RHON ) RHONE POULENC RORER PHARM INC.
XX Maciag T, Burgess W;
XX WPI; 1996-412132/41.
XX N-PSDB; AAT37503.
XX Isolated, purified, biologically active bovine beta endothelial cell
XX growth factor - useful to regenerate or treat damaged blood vessels.
XX Disclosure; Fig 8; 28pp; English.
XX Bovine beta-endothelial cell growth factor (beta-ECGF; AAW03999) having a
XX mol. wt. of 20 kD can be purified at least 16300 fold from bovine brain
XX using heparin-Sepharose affinity chromatography. ECGF is useful for,
XX among other purposes, diagnostic applications and has potential in the
XX treatment of damaged blood vessels or other endothelial cell-lined
XX structures. Human ECGF (AAT37503) or fragments may be obtained using
XX oligonucleotides (AAT37504 and AAT37508 to AAT37509) whose design is
XX based on the sequence of bovine alpha- and beta-ECGF. (Updated on 25-MAR-
XX 2003 to correct PF field.)
XX Sequence 154 AA;
SQ
Query Match 99.3%; Score 757; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 7e-78;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHILQLLSAESVGEVYIKSTE 61
DB 15 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHILQLLSAESVGEVYIKSTE 74
QY 62 TGOYLAMDTDGLLYGSGQTPNEECFLERLEENHYNTYISKHAEKNWVGLKKGSCRRG 121
DB 75 TGOYLAMDTDGLLYGSGQTPNEECFLERLEENHYNTYISKHAEKNWVGLKKGSCRRG 134
QY 122 PRTHYGQKAILFLPLPVSSD 141
DB 135 PRTHYGQKAILFLPLPVSSD 154
RESULT 13
AAW06816
ID AAW06816 standard; protein; 154 AA.
XX AAW06816;
XX 25-MAR-2003 (revised)
XX 17-MAR-1997 (first entry)
XX Human endothelial cell growth factor-beta.
XX Endothelial cell growth factor-beta; ECGF-beta.
XX Homo sapiens.
XX US571790-A.
XX 05-NOV-1996.
PD
XX PF 04-NOV-1996; 96US-00743261.
XX PR 03-MAR-1986; 86US-00835594.
XX
XX PF 07-JUN-1995; 95US-00472964.
XX 03-MAR-1986; 86US-00835594.
XX 18-DEC-1987; 87US-00134499.
XX 29-APR-1991; 91US-00693079.
XX 27-NOV-1991; 91US-00799859.
XX 03-NOV-1994; 94US-00334884.
XX (RHON ) RHONE POULENC RORER PHARM INC.
XX Drohan WN, Jaye M, Maciag T, Burgess W;
XX WPI; 1996-505421/50.
XX N-PSDB; AAT45983.
XX Recombinant human endothelial cell growth factors - for treating damaged
XX blood vessels, etc.
XX Claim 1; Col 16; 22pp; English.
XX Human recombinant endothelial cell growth factors (ECGF) beta (AAW06816)
XX and alpha (AAW06817) differ only at their N-terminal ends. They can be
XX produced in transformed prokaryotic or eukaryotic host cells using DNA
XX sequences (AAT45983 and AAT45984, respectively) derived from the complete
XX human ECGF cDNA (AAT45985). Large quantities of the ECGFs are produced by
XX culturing the host cells and recovering the proteins. ECGFs have utility
XX in the growth and amplification of endothelial cells in culture. They can
XX potentially be used to treat damaged blood vessels and other endothelial
XX cell-lined structures, and also have diagnostic applns. (Updated on 25-
XX MAR-2003 to correct PF field.)
XX Sequence 154 AA;
SQ
Query Match 99.3%; Score 757; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 7e-78;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHILQLLSAESVGEVYIKSTE 61
DB 15 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHILQLLSAESVGEVYIKSTE 74
QY 62 TGOYLAMDTDGLLYGSGQTPNEECFLERLEENHYNTYISKHAEKNWVGLKKGSCRRG 121
DB 75 TGOYLAMDTDGLLYGSGQTPNEECFLERLEENHYNTYISKHAEKNWVGLKKGSCRRG 134
QY 122 PRTHYGQKAILFLPLPVSSD 141
DB 135 PRTHYGQKAILFLPLPVSSD 154
RESULT 14
AAW75414
ID AAW75414 standard; protein; 154 AA.
XX AAW75414;
XX 02-MAR-1999 (first entry)
XX Human beta-endothelial cell growth factor.
XX Human; endothelial cell growth factor; ECGF; brain stem; probe;
XX hybridisation; bovine; wound healing; prosthetic device.
XX Homo sapiens.
XX US5827826-A.
XX 27-OCT-1998.
XX 04-NOV-1996; 96US-00743261.
XX 03-MAR-1986; 86US-00835594.
XX

```

```
PR 18-DEC-1987; 87US-00134499.
PR 29-APR-1991; 91US-00693079.
PR 27-NOV-1991; 91US-00799859.
PR 03-NOV-1994; 94US-00334884.
PR 07-JUN-1995; 95US-00472964.
XX
FA (RHON ) RHONE-POULENC RORER PHARM INC.
XX
PI Jaye M, Burgess W, Maciag T, Drohan WN;
XX
DR WPI; 1998-594032/50.
XX
PT Compositions for promoting wound healing - containing endothelial cell
PT growth factor polypeptides.
XX
PS Claim 1; Col 16; 23pp; English.
XX
CC This sequence represents the amino acid sequence of the mature human beta
CC -endothelial cell growth factor (b-ECGF). This amino acid sequence is
CC identical to the alpha-ECGF but the beta sequence contains an extra 20 N-
CC terminal amino acids. The sequence was isolated from a human brain stem
CC cell cDNA library using a probe designed based on fragments of the bovine
CC ECGF (see AA75416-W75418). The ECGF protein can be used in compositions
CC for promoting wound healing. ECGF is also used to grow cells on a
CC prosthetic device
XX
SQ Sequence 154 AA;
Query Match 99.3%; Score 757; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 7e-78;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
Db 15 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 74
Qy 62 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKKHAENWVGLKKNKSGCKRG 121
Db 75 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKKHAENWVGLKKNKSGCKRG 134
Qy 122 PRTHYGQKAILFLPLPVSSD 141
Db 135 PRTHYGQKAILFLPLPVSSD 154
RESULT 15
AAW92283
ID AAW92283 standard; protein; 154 AA.
XX
AC AAW92283;
XX
DT 20-APR-1999 (first entry)
XX
DE Human beta-endothelial cell growth factor (ECGF) protein sequence.
XX
KW Endothelial cell growth factor; ECGF; cleavable; recombinant; repair;
KW regenerate; blood vessel; endothelial cell; human.
XX
OS Homo sapiens.
XX
FN US5949538-A.
XX
PD 15-DEC-1998.
XX
DF 11-APR-1997; 97US-00840088.
XX
PR 03-MAR-1986; 86US-00835594.
PR 18-DEC-1987; 87US-00134499.
PR 29-APR-1991; 91US-00693079.
PR 27-NOV-1991; 91US-00799859.
PR 03-NOV-1994; 94US-00334884.
PR 07-JUN-1995; 95US-00472964.
PR 04-NOV-1996; 96US-00743261.
```

```
XX
FA (RHON ) RHONE-POULENC RORER PHARM INC.
XX
PI Jaye M, Burgess W, Maciag T, Drohan WN;
XX
DR WPI; 1999-069734/06.
XX
PT DNA encoding a cleavable signal peptide and an endothelial cell growth
PT factor - useful for producing recombinant endothelial cell growth factor
PT proteins.
XX
PS Claim 1; Col 16; 23pp; English.
XX
CC This represents the amino acid sequence of human beta-endothelial cell
CC growth factor (ECGF). The invention is directed to DNA encoding alpha- or
CC beta-ECGF and plasmids comprising the DNA sequences. The DNA encodes a
CC cleavable signal peptide and an ECGF, where removal of the signal peptide
CC yields a mature form of the ECGF. The DNA is used to produce recombinant
CC ECGF proteins, which can be used in treatments to repair or regenerate
CC blood vessels or other structures lined with endothelial cells
XX
SQ Sequence 154 AA;
Query Match 99.3%; Score 757; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 7e-78;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
Db 15 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 74
Qy 62 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKKHAENWVGLKKNKSGCKRG 121
Db 75 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKKHAENWVGLKKNKSGCKRG 134
Qy 122 PRTHYGQKAILFLPLPVSSD 141
Db 135 PRTHYGQKAILFLPLPVSSD 154
Search completed: June 6, 2005, 07:45:30
Job time : 110.561 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 6, 2005, 07:37:42 ; Search time 28.5811 seconds
(without alignments)
368.269 Million cell updates/sec

Title: US-10-649-480A-7

Perfect score: 762

Sequence: 1 MFNLPNGYKPKLLYCSNG.....PRTHYGOKAILFLPLPVSSD 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pgp:*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pgp:*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pgp:*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pgp:*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pgp:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pgp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	762	100.0	141	4	US-09-929-945-7
2	762	100.0	141	4	US-09-929-918-7
3	757	99.3	140	1	US-07-830-330-6
4	757	99.3	140	6	5464943-28
5	757	99.3	140	6	5464943-28
6	757	99.3	154	4	US-09-929-945-8
7	757	99.3	155	1	US-08-439-725A-9
8	757	99.3	155	1	US-08-464-590A-13
9	757	99.3	155	1	US-08-462-169B-9
10	757	99.3	155	2	US-08-207-412B-8
11	757	99.3	155	2	US-08-867-471-9
12	757	99.3	155	2	US-08-951-822-29
13	757	99.3	155	3	US-09-103-079-9
14	757	99.3	155	3	US-08-705-245-5
15	757	99.3	155	3	US-08-718-904-10
16	757	99.3	155	3	US-09-023-082A-16
17	757	99.3	155	3	US-09-093-585-13
18	757	99.3	155	3	US-09-098-628-4
19	757	99.3	155	3	US-09-368-951-29
20	757	99.3	155	4	US-09-425-021-9
21	757	99.3	155	4	US-09-449-249-10
22	757	99.3	155	4	US-09-390-207-14
23	757	99.3	155	4	US-09-229-947-29
24	757	99.3	155	4	US-09-564-829-3
25	757	99.3	155	4	US-09-248-998-16
26	757	99.3	155	4	US-09-572-406B-7
27	757	99.3	155	4	US-09-490-714-5

28	757	99.3	155	4	US-09-929-945-2	Sequence 2, Appli
29	757	99.3	155	4	US-09-610-651-16	Sequence 16, Appli
30	757	99.3	155	4	US-09-929-918-2	Sequence 2, Appli
31	757	99.3	155	4	US-09-929-918-11	Sequence 11, Appli
32	755	99.1	155	2	US-08-438-439C-13	Sequence 13, Appli
33	746.5	98.0	156	3	US-09-030-613-15	Sequence 15, Appli
34	746.5	98.0	156	3	US-09-451-905-15	Sequence 15, Appli
35	734.5	96.4	191	2	US-08-438-439C-22	Sequence 22, Appli
36	732	96.1	140	4	US-09-417-721-1	Sequence 1, Appli
37	732	96.1	140	4	US-09-377-675A-8	Sequence 8, Appli
38	730	95.8	155	4	US-09-390-207-24	Sequence 24, Appli
39	727	95.4	136	6	5437995-2	Patent No. 5437995
40	727	95.4	136	6	5437995-2	Patent No. 5437995
41	721	94.6	135	4	US-09-929-945-5	Sequence 5, Appli
42	721	94.6	135	4	US-09-929-918-5	Sequence 5, Appli
43	697	91.5	140	1	US-07-830-330-7	Sequence 7, Appli
44	697	91.5	140	1	US-08-187-780-4	Sequence 4, Appli
45	697	91.5	140	2	US-08-478-485-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-929-945-7
; Sequence 7, Application US/09929945
; Patent No. 6642026
; GENERAL INFORMATION:
; APPLICANT: Stegmann, Thomas
; APPLICANT: Kordyum, Vitaliy A.
; APPLICANT: Chernykh, Svitlana I.
; APPLICANT: Slavchenko, Iryna Yu.
; APPLICANT: Vozianov, Oleksandr
; TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR 155
; FILE REFERENCE: CVGENG.008A
; CURRENT APPLICATION NUMBER: US/09/929,945
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-929-945-7

Query Match	100.0%	Score 762;	DB 4;	Length 141;
Best Local Similarity	100.0%	Pred. No. 1.3e-80;		
Matches 141;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MFNLPNGYKPKLLYCSNGGHFLRLPDGTGVDGTRDRSDQHIQLQLSAESVGEVYIKST	60	
Db	1	MFNLPNGYKPKLLYCSNGGHFLRLPDGTGVDGTRDRSDQHIQLQLSAESVGEVYIKST	60	
QY	61	ETGOVLANDTGLLYGSGTNPNECLFLERLENHNTYISKHAEKNMFVGLKNGSKCR	120	
Db	61	ETGOVLANDTGLLYGSGTNPNECLFLERLENHNTYISKHAEKNMFVGLKNGSKCR	120	
QY	121	GPRTHYGOKAILFLPLPVSSD	141	
Db	121	GPRTHYGOKAILFLPLPVSSD	141	

RESULT 2
US-09-929-918-7
; Sequence 7, Application US/09929918
; Patent No. 6773899
; GENERAL INFORMATION:
; APPLICANT: Kordyum, Vitaliy A.
; APPLICANT: Chernykh, Svitlana I.
; APPLICANT: Slavchenko, Iryna Yu.
; APPLICANT: Vozianov, Oleksandr
; TITLE OF INVENTION: PHAGE-DEPENDENT SUPER PRODUCTION OF

; TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN AND PEPTIDES
; FILE REFERENCE: PHAGE.006A
; CURRENT APPLICATION NUMBER: US/09/929,918
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 09/318,288
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Translated protein sequence for the chemically
; OTHER INFORMATION: synthesized 140 amino acid form of fibroblast
; OTHER INFORMATION: growth factor
US-09-929-918-7

Query Match 100.0%; Score 762; DB 4; Length 141;
Best Local Similarity 100.0%; Pred. No. 1.3e-80;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFNLPPGNYKKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHIQLLSAESVGEVYIKST 60
Db 1 MFNLPPGNYKKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHIQLLSAESVGEVYIKST 60

Qy 61 ETGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAEKNWVGLKKGCKR 120
Db 61 ETGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAEKNWVGLKKGCKR 120

Qy 121 GPRTHYGOKAILFLPLPVSSD 141
Db 121 GPRTHYGOKAILFLPLPVSSD 141

RESULT 3
US-07-830-330-6
; Sequence 6, Application US/07830330
; Patent No. 5288704
; GENERAL INFORMATION:
; APPLICANT: Ungheri, Domenico
; APPLICANT: Garofano, Luisa
; APPLICANT: Battistini, Carlo
; APPLICANT: Carminati, Paolo
; APPLICANT: Mazue, Guy
; TITLE OF INVENTION: SYNERGISTIC COMPOSITION COMPRISING A
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR AND A SULFATED POLYSACCHARIDE,
; TITLE OF INVENTION: FOR USE AS ANTI-VIRAL AGENT
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ORLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C. STREET, 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/830,330
; FILING DATE: 19920420
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5288704man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 769-230-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-07-830-330-6

Query Match 99.3%; Score 757; DB 1; Length 140;
Best Local Similarity 100.0%; Pred. No. 4.9e-80;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHIQLLSAESVGEVYIKSTE 61
Db 1 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHIQLLSAESVGEVYIKSTE 60

Qy 62 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAEKNWVGLKKGCKR 121
Db 61 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAEKNWVGLKKGCKR 120

Qy 122 PRTHYGOKAILFLPLPVSSD 141
Db 121 PRTHYGOKAILFLPLPVSSD 140

RESULT 4
5464943-28
; Patent No. 5464943
; APPLICANT: SENOO, MASAHARU,SASADA, REIKO;IGARASHI, KOICHI
; TITLE OF INVENTION: DNA ENCODING GLYCOSYLATED FGF AND
; PRODUCTION THEREOF
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/275,635
; FILING DATE: 15-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 7,089
; FILING DATE: 19-JAN-1993
; APPLICATION NUMBER: 511,469
; FILING DATE: 20-APR-1990
; SEQ ID NO:28;
; LENGTH: 140
5464943-28

Query Match 99.3%; Score 757; DB 6; Length 140;
Best Local Similarity 100.0%; Pred. No. 4.9e-80;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHIQLLSAESVGEVYIKSTE 61
Db 1 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHIQLLSAESVGEVYIKSTE 60

Qy 62 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAEKNWVGLKKGCKR 121
Db 61 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAEKNWVGLKKGCKR 120

Qy 122 PRTHYGOKAILFLPLPVSSD 141
Db 121 PRTHYGOKAILFLPLPVSSD 140

RESULT 5
5464943-28
; Patent No. 5464943
; APPLICANT: SENOO, MASAHARU,SASADA, REIKO;IGARASHI, KOICHI
; TITLE OF INVENTION: DNA ENCODING GLYCOSYLATED FGF AND
; PRODUCTION THEREOF
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/275,635
; FILING DATE: 15-JUL-1994

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 7,089
; FILING DATE: 19-JAN-1993
; APPLICATION NUMBER: 511,469
; FILING DATE: 20-APR-1990
; SEQ ID NO:28
; LENGTH: 140
5464943-28

Query Match      99.3%; Score 757; DB 6; Length 140;
Best Local Similarity 100.0%; Pred. No. 4.9e-80;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FNLPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
Db 1 FNLPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 60

Qy 62 TQOYLAMDTDGLLYGSQTPNEECFLERLEENHNHYTIYSKKHAEKNWVFLGLKKGSCCKRG 121
Db 61 TQOYLAMDTDGLLYGSQTPNEECFLERLEENHNHYTIYSKKHAEKNWVFLGLKKGSCCKRG 120

Qy 122 PRTHYGQKAILFLPLPVSSD 141
Db 121 PRTHYGQKAILFLPLPVSSD 140

RESULT 6
US-09-929-945-8
; Sequence 8, Application US/09929945
; Patent No. 6642026
; GENERAL INFORMATION:
; APPLICANT: Stegmann, Thomas
; APPLICANT: Kordyum, Vitaliy A.
; APPLICANT: Chernykh, Svitlana I.
; APPLICANT: Slavchenko, Iryna Yu.
; APPLICANT: Vozianov, Oleksandr
; TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR 155
; FILE REFERENCE: CVGENG.008A
; CURRENT APPLICATION NUMBER: US/09/929,945
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-929-945-8

Query Match      99.3%; Score 757; DB 4; Length 154;
Best Local Similarity 100.0%; Pred. No. 5.6e-80;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FNLPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
Db 15 FNLPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 74

Qy 62 TQOYLAMDTDGLLYGSQTPNEECFLERLEENHNHYTIYSKKHAEKNWVFLGLKKGSCCKRG 121
Db 75 TQOYLAMDTDGLLYGSQTPNEECFLERLEENHNHYTIYSKKHAEKNWVFLGLKKGSCCKRG 134

Qy 122 PRTHYGQKAILFLPLPVSSD 141
Db 135 PRTHYGQKAILFLPLPVSSD 154

RESULT 7
US-08-439-725A-9
; Sequence 9, Application US/08439725A
; Patent No. 5693775
; GENERAL INFORMATION:
; APPLICANT: Nathans, Jeremy
; APPLICANT: Smallwood, Philip M.
```

```
; APPLICANT: Macke, Jennifer P.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS
; TITLE OF INVENTION: FACTOR-1 (FHF-1) AND METHODS OF USE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,725A
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/047001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 617/678-5099
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 155 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-439-725A-9

Query Match      99.3%; Score 757; DB 1; Length 155;
Best Local Similarity 100.0%; Pred. No. 5.6e-80;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FNLPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
Db 16 FNLPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 75

Qy 62 TQOYLAMDTDGLLYGSQTPNEECFLERLEENHNHYTIYSKKHAEKNWVFLGLKKGSCCKRG 121
Db 76 TQOYLAMDTDGLLYGSQTPNEECFLERLEENHNHYTIYSKKHAEKNWVFLGLKKGSCCKRG 135

Qy 122 PRTHYGQKAILFLPLPVSSD 141
Db 136 PRTHYGQKAILFLPLPVSSD 155

RESULT 8
US-08-464-590A-13
; Sequence 13, Application US/08464590A
; Patent No. 5763214
; GENERAL INFORMATION:
; APPLICANT: HU, JING-SHAN
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR-11
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESSEE: STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NJ
; COUNTRY: US
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,590A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J. G.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 325800-438
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 994-1700
TELEFAX: (201) 994-1744
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 155 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-590A-13

Query Match 99.3%; Score 757; DB 1; Length 155;
Best Local Similarity 100.0%; Pred. No. 5.6e-80;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
Db 16 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 75

Qy 62 TGQYLAAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAENKWFVGLKKGSKCRG 121
Db 76 TGQYLAAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAENKWFVGLKKGSKCRG 135

Qy 122 PRTHYGQKAILFLPLPVSSD 141
Db 136 PRTHYGQKAILFLPLPVSSD 155

RESULT 9
US-08-462-169B-9
Sequence 9, Application US/08462169B
Patent No. 5773252
GENERAL INFORMATION:
APPLICANT: John Greene and Craig A. Rosen
TITLE OF INVENTION: Fibroblast Growth Factor-15
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,169B
FILING DATE: 05 JUN 95
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-441 (PF203)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:

LENGTH: 155 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-462-169B-9

Query Match 99.3%; Score 757; DB 1; Length 155;
Best Local Similarity 100.0%; Pred. No. 5.6e-80;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
Db 16 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 75

Qy 62 TGQYLAAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAENKWFVGLKKGSKCRG 121
Db 76 TGQYLAAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAENKWFVGLKKGSKCRG 135

Qy 122 PRTHYGQKAILFLPLPVSSD 141
Db 136 PRTHYGQKAILFLPLPVSSD 155

RESULT 10
US-08-207-412B-8
Sequence 8, Application US/08207412B
Patent No. 5817485
GENERAL INFORMATION:
APPLICANT: Hu, Jing-Shan
TITLE OF INVENTION: Fibroblast Growth Factor-10
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: USA
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/207,412B
FILING DATE: 08-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 155 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-207-412B-8

Query Match 99.3%; Score 757; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 5.6e-80;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
Db 16 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 75

Qy 122 PRTHYGKAILFLPLPVSSD 141
|
Db 136 PRTHYGKAILFLPLPVSSD 155

RESULT 14

US-08-705-245-5
; Sequence 5, Application US/08705245
; Patent No. 6020189
; GENERAL INFORMATION:
; APPLICANT: Nathans et al., Jeremy
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS
; TITLE OF INVENTION: FACTORS (FHFes) AND METHODS OF USE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/705,245
; FILING DATE: 30-AUG-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: 07265/094001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-50999
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 155 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-705-245-5

Query Match 99.3%; Score 757; DB 3; Length 155;
Best Local Similarity 100.0%; Pred. No. 5.6e-80;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
|
Db 16 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 75
|
Qy 62 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAENWVGLKKGSCCKRG 121
|
Db 76 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAENWVGLKKGSCCKRG 135
|
Qy 122 PRTHYGKAILFLPLPVSSD 141
|
Db 136 PRTHYGKAILFLPLPVSSD 155

RESULT 15

US-08-718-904-10
; Sequence 10, Application US/08718904
; Patent No. 6037329
; GENERAL INFORMATION:
; APPLICANT: Baird, J. Andrew
; APPLICANT: Chandler, Lois Ann
; APPLICANT: Sosnowski, Barbara A.
; TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPE
; NUMBER OF SEQUENCES: 128

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/718,904
; FILING DATE: 24-SEP-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6037329tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 760100.415C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 155 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: /note= "FGF-1"
; US-08-718-904-10

Query Match 99.3%; Score 757; DB 3; Length 155;
Best Local Similarity 100.0%; Pred. No. 5.6e-80;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
|
Db 16 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 75
|
Qy 62 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAENWVGLKKGSCCKRG 121
|
Db 76 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAENWVGLKKGSCCKRG 135
|
Qy 122 PRTHYGKAILFLPLPVSSD 141
|
Db 136 PRTHYGKAILFLPLPVSSD 155

Search completed: June 6, 2005, 07:47:28
Job time : 28.5811 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 6, 2005, 07:37:37 ; Search time 22.8649 Seconds

(without alignments)
593.337 Million cell updates/sec

Title: US-10-649-480A-7

Perfect score: 762

Sequence: 1 MFNLPPGNYKKPKLLYCSNG.....PRTHYGQKAILFLPLPVSSD 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	757	99.3	155	1 A33665	acidic fibroblast
2	744	97.6	155	1 A60721	acidic fibroblast
3	730	95.8	155	2 D37360	acidic fibroblast
4	730	95.8	155	2 S04147	acidic fibroblast
5	727	95.4	152	2 JH0476	acidic fibroblast
6	697	91.5	155	1 GK80A	acidic fibroblast
7	689	90.4	155	2 JW0055	acidic fibroblast
8	678	89.0	155	2 A60130	acidic fibroblast
9	395	51.8	146	1 S00185	basic fibroblast g
10	395	51.8	157	1 GK80B	basic fibroblast g
11	394	51.7	189	2 A48834	basic fibroblast g
12	389	51.0	154	2 C37360	basic fibroblast g
13	389	51.0	154	2 A31674	basic fibroblast g
14	386	50.7	210	2 A32398	basic fibroblast g
15	380	49.9	164	2 S31622	basic fibroblast g
16	364	47.8	155	1 A40117	basic fibroblast g
17	361	47.4	137	2 I46711	fibroblast growth
18	251	32.9	211	2 JC7353	fibroblast growth
19	250	32.8	212	2 JC7511	fibroblast growth
20	249.5	32.7	208	2 S66486	fibroblast growth
21	249.5	32.7	208	2 A48137	fibroblast growth
22	247.5	32.5	208	2 JC7082	fibroblast somatot
23	244.5	32.1	207	2 JC5941	fibroblast growth
24	240.5	31.6	207	2 JC5940	fibroblast growth
25	237.5	31.2	256	2 JC4627	fibroblast growth
26	232	30.4	60	2 JH0708	fibroblast growth
27	231.5	30.4	220	2 I50588	fibroblast growth
28	228.5	30.0	237	1 S39582	transforming prote
29	219	28.7	245	1 TVN5T2	

30	214	28.1	239	1 S04742	fibroblast growth
31	211	27.7	187	2 S23595	embryonic fibrobla
32	208.5	27.4	194	2 S49501	keratinocyte growt
33	206.5	27.1	194	2 I48610	keratinocyte growt
34	204.5	26.8	194	1 A36301	fibroblast growth
35	204.5	26.8	194	2 S26049	fibroblast growth
36	201.5	26.4	168	2 JG0184	fibroblast growth
37	201	26.4	192	2 S54407	embryonic fibrobla
38	200	26.2	264	2 A36207	fibroblast growth
39	200	26.2	266	2 S88144	fibroblast growth
40	198	26.0	194	2 I50710	fibroblast growth
41	197.5	25.9	413	2 H88481	protein let-756 (l
42	195	25.6	267	1 TVHUF5	fibroblast growth
43	191.5	25.1	125	2 A32484	basic fibroblast g
44	188	24.7	206	2 JC4268	fibroblast growth
45	185	24.3	206	1 TVHUM5	fibroblast growth

ALIGNMENTS

RESULT 1

A33665

acidic fibroblast growth factor 1 precursor [validated] - human

N:Alternate names: beta-ECGF; endothelial cell growth factor beta; heparin-binding growth

C:Species: Homo sapiens (man)

C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004

C:Accession: A33665; A32316; S18217; A43804; A24662; JH0707; S35335; S35336; I39413; A23:

R:Merxia, A.; Tischer, E.; Graves, D.; Tumolo, A.; Miller, J.; Gospodarowicz, D.; Abrah

Biochem. Biophys. Res. Commun. 164, 1121-1129, 1989

A:Title: Structural analysis of the gene for human acidic fibroblast growth factor.

A:Reference number: A33665; MUID:90073637; PMID:2590193

A:Accession: A33665

A:Molecule type: DNA

A:Residues: 1-155 <MER>

A:Cross-references: UNIPROT:P05230; GB:M30491

R:Wang, W.P.; Lehtoma, K.; Varban, M.L.; Krishnan, I.; Chiu, I.M.

Mol. Cell. Biol. 9, 2387-2395, 1989

A:Title: Cloning of the gene coding for human class 1 heparin-binding growth factor and

A:Reference number: A32316; MUID:89343957; PMID:2474753

A:Accession: A32316

A:Molecule type: DNA

A:Residues: 1-155 <WAN>

A:Cross-references: GB:M23087; NID:G183875; PIDN:AAA52638.1; PID:G386768

R:Wang, W.P.; Quick, D.; Balcerzak, S.P.; Needelman, S.W.; Chiu, I.M.

30	214	28.1	239	1 S04742	fibroblast growth
31	211	27.7	187	2 S23595	embryonic fibrobla
32	208.5	27.4	194	2 S49501	keratinocyte growt
33	206.5	27.1	194	2 I48610	keratinocyte growt
34	204.5	26.8	194	1 A36301	fibroblast growth
35	204.5	26.8	194	2 S26049	fibroblast growth
36	201.5	26.4	168	2 JG0184	fibroblast growth
37	201	26.4	192	2 S54407	embryonic fibrobla
38	200	26.2	264	2 A36207	fibroblast growth
39	200	26.2	266	2 S88144	fibroblast growth
40	198	26.0	194	2 I50710	fibroblast growth
41	197.5	25.9	413	2 H88481	protein let-756 (l
42	195	25.6	267	1 TVHUF5	fibroblast growth
43	191.5	25.1	125	2 A32484	basic fibroblast g
44	188	24.7	206	2 JC4268	fibroblast growth
45	185	24.3	206	1 TVHUM5	fibroblast growth

ALIGNMENTS

RESULT 1

A33665

acidic fibroblast growth factor 1 precursor [validated] - human

N:Alternate names: beta-ECGF; endothelial cell growth factor beta; heparin-binding growth

C:Species: Homo sapiens (man)

C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004

C:Accession: A33665; A32316; S18217; A43804; A24662; JH0707; S35335; S35336; I39413; A23:

R:Merxia, A.; Tischer, E.; Graves, D.; Tumolo, A.; Miller, J.; Gospodarowicz, D.; Abrah

Biochem. Biophys. Res. Commun. 164, 1121-1129, 1989

A:Title: Structural analysis of the gene for human acidic fibroblast growth factor.

A:Reference number: A33665; MUID:90073637; PMID:2590193

A:Accession: A33665

A:Molecule type: DNA

A:Residues: 1-155 <MER>

A:Cross-references: UNIPROT:P05230; GB:M30491

R:Wang, W.P.; Lehtoma, K.; Varban, M.L.; Krishnan, I.; Chiu, I.M.

Mol. Cell. Biol. 9, 2387-2395, 1989

A:Title: Cloning of the gene coding for human class 1 heparin-binding growth factor and

A:Reference number: A32316; MUID:89343957; PMID:2474753

A:Accession: A32316

A:Molecule type: DNA

A:Residues: 1-155 <WAN>

A:Cross-references: GB:M23087; NID:G183875; PIDN:AAA52638.1; PID:G386768

R:Wang, W.P.; Quick, D.; Balcerzak, S.P.; Needelman, S.W.; Chiu, I.M.

30	214	28.1	239	1 S04742	fibroblast growth
31	211	27.7	187	2 S23595	embryonic fibrobla
32	208.5	27.4	194	2 S49501	keratinocyte growt
33	206.5	27.1	194	2 I48610	keratinocyte growt
34	204.5	26.8	194	1 A36301	fibroblast growth
35	204.5	26.8	194	2 S26049	fibroblast growth
36	201.5	26.4	168	2 JG0184	fibroblast growth
37	201	26.4	192	2 S54407	embryonic fibrobla
38	200	26.2	264	2 A36207	fibroblast growth
39	200	26.2	266	2 S88144	fibroblast growth
40	198	26.0	194	2 I50710	fibroblast growth
41	197.5	25.9	413	2 H88481	protein let-756 (l
42	195	25.6	267	1 TVHUF5	fibroblast growth
43	191.5	25.1	125	2 A32484	basic fibroblast g
44	188	24.7	206	2 JC4268	fibroblast growth
45	185	24.3	206	1 TVHUM5	fibroblast growth

ALIGNMENTS

RESULT 1

A33665

acidic fibroblast growth factor 1 precursor [validated] - human

N:Alternate names: beta-ECGF; endothelial cell growth factor beta; heparin-binding growth

C:Species: Homo sapiens (man)

C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004

C:Accession: A33665; A32316; S18217; A43804; A24662; JH0707; S35335; S35336; I39413; A23:

R:Merxia, A.; Tischer, E.; Graves, D.; Tumolo, A.; Miller, J.; Gospodarowicz, D.; Abrah

Biochem. Biophys. Res. Commun. 164, 1121-1129, 1989

A:Title: Structural analysis of the gene for human acidic fibroblast growth factor.

A:Reference number: A33665; MUID:90073637; PMID:2590193

A:Accession: A33665

A:Molecule type: DNA

A;Molecule type: mRNA
A;Residues: 1-155 <YU>
A;Cross-references: GB:X65778; NID:G396163; PIDN:CAA46661.1; PID:G396164
R;Payson, R.A.; Canatani, H.; Chotani, M.A.; Wang, W.P.; Harris, S.E.; Myers, R.L.; Chiu, Nucleic Acids Res. 21, 489-495, 1993
A;Title: Cloning of two novel forms of human acidic fibroblast growth factor (aFGF) mRNA
A;Reference number: S35535; MUID:93181239; PMID:7680120
A;Accession: S35535
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-58 <PAY>
A;Cross-references: GB:L01485
A;Accession: S35536
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-58 <PA2>
A;Cross-references: GB:L01487
R;Crumley, G.; Dionne, C.A.; Jaye, M., Biochem. Biophys. Res. Commun. 171, 7-13, 1990
A;Title: The gene for human acidic fibroblast growth factor encodes two upstream exons and a 3' untranslated region
A;Reference number: I39412; MUID:90365758; PMID:2393407
A;Accession: I39413
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-40 <RES>
A;Cross-references: GB:M60515; NID:G178226; PIDN:AAA51672.1; PID:G553170; GB:M60516; NID:G178226
R;Harper, J.W.; Strydom, D.J.; Lobb, R.R. Biochemistry 25, 4097-4103, 1986
A;Reference number: A23553; MUID:86296647; PMID:2427112
A;Accession: A23553
A;Molecule type: protein
A;Residues: 16-155 <HAR>
R;Gimenez-Gallego, G.; Conn, G.; Hatcher, V.B.; Thomas, K.A. Biochem. Biophys. Res. Commun. 138, 611-617, 1986
A;Title: The complete amino acid sequence of human brain-derived acidic fibroblast growth factor
A;Reference number: A24820; MUID:86295741; PMID:3527167
A;Accession: A24820
A;Molecule type: protein
A;Residues: 16-155 <GIM>
R;Gimenez-Gallego, G.; Conn, G.; Hatcher, V.B.; Thomas, K.A. Biochem. Biophys. Res. Commun. 135, 541-548, 1986
A;Title: Human brain-derived acidic and basic fibroblast growth factors: amino terminal regions are identical
A;Reference number: A90122; MUID:86186784; PMID:3964259
A;Accession: A24243
A;Molecule type: protein
A;Residues: 16-47 <GI2>
A;Experimental source: brain
R;Gautschi, P.; Frater-Schroder, M.; Bohlen, P. FEBS Lett. 204, 203-207, 1986
A;Title: Partial molecular characterization of endothelial cell mitogens from human brain
A;Reference number: A91364; MUID:86275260; PMID:3732516
A;Accession: A24301
A;Molecule type: protein
A;Residues: 16-30, 'X', 32-49 <GAU>
R;Gautschi-Sova, P.; Muller, T.; Bohlen, P. Biochem. Biophys. Res. Commun. 140, 874-880, 1986
A;Title: Amino acid sequence of human acidic fibroblast growth factor.
A;Reference number: A26386; MUID:87048871; PMID:3778488
A;Accession: A26386
A;Molecule type: protein
A;Residues: 16-155 <GA2>
A;Experimental source: brain
R;Chavan, A.J.; Haley, B.E.; Volkin, D.B.; Marfia, K.E.; Verticelli, A.M.; Bruner, M.W.; Biochemistry 33, 7193-7202, 1994
A;Title: Interaction of nucleotides with acidic fibroblast growth factor (FGF-1).
A;Reference number: A53639; MUID:94271773; PMID:7516183
A;Accession: A53639
A;Molecule type: protein
A;Residues: 16-30, 'X', 32-38; 73-75, 'X', 77-97, 'X', 99-101; 128-131, 'X', 133-140, 'X', 142-152 <FGF1>
C;Genetics:
A;Gene: GDB:FGF1; FGFA
A;Cross-references: GDB:I19909; OMIM:131220
A;Map position: 5q31.3-5q33.2

A;Introns: 57/1; 91/3
C;Superfamily: fibroblast growth factor
C;Keywords: alternative splicing; growth factor; heparin binding
F;16-155/Product: fibroblast growth factor 1 #status experimental <MAT>
F;129/Binding site: carbohydrate (Asn) (covalent) #status absent
Query Match 99.3%; Score 757; DB 1; Length 155;
Best Local Similarity 100.0%; Pred. No. 4.1e-65;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
Db 16 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 75
QY 62 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKKHAENKMFVGLKKGSCCKRG 121
Db 76 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKKHAENKMFVGLKKGSCCKRG 135
QY 122 PRTHYGOKAILFLPLPVSSD 141
Db 136 PRTHYGOKAILFLPLPVSSD 155
RESULT 2
A60721
acidic fibroblast growth factor - golden hamster
N;Alternate names: heparin-binding growth factor 1
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A60721
R;Hall, J.A.; Harris, M.A.; Malark, M.; Mansson, P.E.; Zhou, H.; Harris, S.E. J. Cell. Biochem. 43, 17-26, 1990
A;Title: Characterization of the hamster DDT-1 cell aFGF/HGBF-I gene and its moc
A;Reference number: A60721; MUID:90270291; PMID:1693366
A;Accession: A60721
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-155 <HAL>
A;Cross-references: UNIPROT:P34004
C;Superfamily: fibroblast growth factor
C;Keywords: growth factor; heparin binding
Query Match 97.6%; Score 744; DB 1; Length 155;
Best Local Similarity 97.9%; Pred. No. 7.2e-64;
Matches 137; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
Db 16 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 75
QY 62 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKKHAENKMFVGLKKGSCCKRG 121
Db 76 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKKHAENKMFVGLKKGSCCKRG 135
QY 122 PRTHYGOKAILFLPLPVSSD 141
Db 136 PRTHYGOKAILFLPLPVSSD 155
RESULT 3
D37360
acidic fibroblast growth factor - mouse
N;Alternate names: aFGF; FGF-1
C;Species: Mus musculus (house mouse)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: D37360; JCS231
R;Hebert, J.M.; Basilico, C.; Goldfarb, M.; Haub, O.; Martin, G.R. Dev. Biol. 138, 454-463, 1990
A;Title: Isolation of cDNAs encoding four mouse FGF family members and characterization
A;Reference number: A37360; MUID:90201563; PMID:2318343
A;Accession: D37360
A;Status: preliminary
A;Molecule type: mRNA

A:Residues: 1-155 <HEB>
A:Cross-references: UNIPROT:P61148; GB:M30641; NID:g193284; PIDN:AAA37618.1; PID:g309236
R:Madiai, F.; Hackshaw, K.V.; Chiu, I.M.
Gene 179, 231-236, 1996
A:Title: Cloning and characterization of the mouse Fgf-1 gene.
A:Reference number: JCS231; MUID:97128312; PMID:8972905
A:Accession: JCS231
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-155 <MAD>
A:Cross-references: GB:U36456
C:Comment: This protein is an inducer of neovascularization in angiogenic disease includ
C:Genetics:
A:Gene: Fgf-1
A:Introns: 57/1, 91/3
C:Superfamily: fibroblast growth factor

Query Match 95.8%; Score 730; DB 2; Length 155;
Best Local Similarity 96.4%; Pred. No. 1.6e-62;
Matches 135; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 FNLPGNYKKPKLLYCSNGGHLRLIPDGTGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
DB 16 FNLPLGNYKKPKLLYCSNGGHLRLIPDGTGTRDRSDQHIQLQLSAESVGEVYIKSTE 75
QY 62 TGOYLAMTDGLLYGSQTPNEECFLERLEENHNYTYSKKHAENKWFVGLKKGSCRRG 121
DB 76 TGOYLAMTEGLLYGSQTPNEECFLERLEENHNYTYSKKHAENKWFVGLKKGSCRRG 135
QY 122 PRTHYGQKAILFLPLPVSSD 141
DB 136 PRTHYGQKAILFLPLPVSSD 155

RESULT 4
S04147
acidic fibroblast growth factor 1 - rat
N:Alternate names: heparin-binding growth factor 1
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C:Accession: S04147
R:Goodrich, S.P.; Yan, G.C.; Bahrenburg, K.; Mansson, P.E.
Nucleic Acids Res. 17, 2867, 1989
A:Title: The nucleotide sequence of rat heparin binding growth factor 1 (HBGF-1).
A:Reference number: S04147; MUID:89240051; PMID:2470029
A:Accession: S04147
A:Molecule type: mRNA
A:Residues: 1-155 <GOO>
A:Cross-references: UNIPROT:P61149; EMBL:X14232; NID:g56351; PIDN:CAA32448.1; PID:g56352
C:Superfamily: fibroblast growth factor
C:Keywords: growth factor; heparin binding

Query Match 95.8%; Score 730; DB 2; Length 155;
Best Local Similarity 96.4%; Pred. No. 1.6e-62;
Matches 135; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 FNLPGNYKKPKLLYCSNGGHLRLIPDGTGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
DB 16 FNLPLGNYKKPKLLYCSNGGHLRLIPDGTGTRDRSDQHIQLQLSAESVGEVYIKSTE 75
QY 62 TGOYLAMTDGLLYGSQTPNEECFLERLEENHNYTYSKKHAENKWFVGLKKGSCRRG 121
DB 76 TGOYLAMTEGLLYGSQTPNEECFLERLEENHNYTYSKKHAENKWFVGLKKGSCRRG 135
QY 122 PRTHYGQKAILFLPLPVSSD 141
DB 136 PRTHYGQKAILFLPLPVSSD 155

RESULT 5
JH0476
acidic fibroblast growth factor - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: JH0476; S20072
R:Schmidt, M.; Sharma, H.S.; Schott, R.J.; Schaper, W.
Biochem. Biophys. Res. Commun. 180, 853-859, 1991
A:Title: Amplification and sequencing of mRNA encoding acidic fibroblast growth factor (a
A:Reference number: JH0476; MUID:92062117; PMID:1719973
A:Accession: JH0476
A:Molecule type: mRNA
A:Residues: 1-152 <SCH>
A:Cross-references: UNIPROT:P20002; EMBL:X60317; NID:g1873; PIDN:CAA42869.1; PID:g1874
A:Experimental source: heart
A:Note: The hydrophobic core residues are packed around the internal symmetry axis
C:Comment: This protein belongs to the fibroblast growth factor family.
C:Superfamily: fibroblast growth factor
C:Keywords: growth factor; heparin binding
F:22-28/Region: nuclear location signal
F:133/Binding site: heparin (Lys) #status predicted

Query Match 95.4%; Score 727; DB 2; Length 152;
Best Local Similarity 97.8%; Pred. No. 3e-62;
Matches 134; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FNLPGNYKKPKLLYCSNGGHLRLIPDGTGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
DB 16 FNLPGNYKKPKLLYCSNGGHLRLIPDGTGTRDRSDQHIQLQLSAESVGEVYIKSTE 75
QY 62 TGOYLAMTDGLLYGSQTPNEECFLERLEENHNYTYSKKHAENKWFVGLKKGSCRRG 121
DB 76 TGOYLAMTEGLLYGSQTPNEECFLERLEENHNYTYSKKHAENKWFVGLKKGSCRRG 135
QY 122 PRTHYGQKAILFLPLPV 138
DB 136 PRTHYGQKAILFLPLPV 152

RESULT 6
GXBOA
acidic fibroblast growth factor precursor - bovine
N:Alternate names: aFGF; eye-derived growth factor II; heparin-binding growth factor I;
C:Species: Bos primigenius taurus (cattle)
C:Date: 13-Aug-1986 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C:Accession: JH0613; S02102; S02661; S22065; B24663; A94281; S03953; A91010; A24477; B25
R:Renaud, F.; Desset, S.; Bugra, K.; Halley, C.; Philippe, J.M.; Courtois, Y.; Laurent, N.
Biochem. Biophys. Res. Commun. 184, 945-952, 1992
A:Title: Heterogeneity of 3' untranslated region of bovine acidic FGF transcripts.
A:Reference number: JH0613; MUID:92246990; PMID:1374244
A:Accession: JH0613
A:Molecule type: DNA
A:Residues: 58-155 <REN>
A:Cross-references: UNIPROT:P03968
R:Halley, C.; Courtois, Y.; Laurent, M.
Nucleic Acids Res. 16, 10913, 1988
A:Title: Nucleotide sequence of bovine acidic fibroblast growth factor cDNA.
A:Reference number: S02102; MUID:89083506; PMID:3205724
A:Accession: S02102
A:Molecule type: mRNA
A:Residues: 1-155 <HAL>
A:Cross-references: EMBL:X13221; NID:g347; PIDN:CAA31610.1; PID:g348
R:Alterio, J.; Halley, C.; Brou, C.; Soussi, T.; Courtois, Y.; Laurent, M.
FEBS Lett. 242, 41-46, 1988
A:Title: Characterization of a bovine acidic FGF cDNA clone and its expression in brain
A:Reference number: S02661; MUID:89078619; PMID:2849564
A:Accession: S02661
A:Molecule type: mRNA
A:Residues: 1-155 <ALT>
A:Cross-references: EMBL:X14032; NID:g322; PIDN:CAA32192.1; PID:g323
R:Philippe, J.M.
Submitted to the EMBL Data Library, May 1992
A:Reference number: S22065
A:Accession: S22065
A:Molecule type: mRNA
A:Residues: 1-18 <PHI>
A:Cross-references: EMBL:X66446; NID:g411; PIDN:CAA47063.1; PID:g412

R;Abraham, J.A.; Mergia, A.; Whang, J.L.; Tumolo, A.; Friedman, J.; Hjerrild, K.A.; Gosp Science 233, 545-548, 1986
A;Title: Nucleotide sequence of a bovine clone encoding the angiogenic protein, basic fi
A;Reference number: A94290; MUID:86261806; PMID:2425435
A;Accession: B24663
A:Molecule type: mRNA
A;Residues: 16-56 <ABR>
R;Gimenez-Gallego, G.; Rodkey, J.; Bennett, C.; Rios-Candelore, M.; DiSalvo, J.; Thomas, Science 230, 1385-1388, 1985
A;Title: Brain-derived acidic fibroblast growth factor: complete amino acid sequence and
A;Reference number: A94281; MUID:86070224; PMID:4071057
A;Accession: A94281
A:Molecule type: protein
A;Residues: 16-155 <GRM>
R;Quinkler, W.; Maasberg, M.; Bernotat-Danielowski, S.; Luethke, N.; Sharma, H.S.; Schape Eur. J. Biochem. 181, 67-73, 1989
A;Title: Isolation of heparin-binding growth factors from bovine, porcine and canine hea
A;Reference number: S03953; MUID:89231704; PMID:2714282
A;Accession: S03953
A:Molecule type: protein
A;Residues: 16-45 <QUT>
R;Bohlen, P.; Esch, F.; Baird, A.; Gospodarowicz, D.
EMBO J. 4, 1951-1956, 1985
A;Title: Acidic fibroblast growth factor (FGF) from bovine brain: amino-terminal sequenc
A;Reference number: A91010; MUID:86055750; PMID:4065099
A;Accession: A91010
A:Molecule type: protein
A;Residues: 16-30, 'X', 32-34, 'X', 36-44 <BOH>
R;Crabb, J.W.; Ames, L.G.; Carr, S.A.; Johnson, C.M.; Roberts, G.D.; Bordoli, R.S.; McK Biochemistry 25, 4988-4993, 1986
A;Title: Complete primary structure of prostatropin, a prostate epithelial cell growth f
A;Reference number: A24477; MUID:87026586; PMID:3768327
A;Accession: A24477
A:Molecule type: protein
A;Residues: 2, 'GE', 5-155 <CRA>
R;Burgess, W.H.; Mehlmann, T.; Marshak, D.R.; Fraser, B.A.; Maciag, T.
Proc. Natl. Acad. Sci. U.S.A. 83, 7216-7220, 1986
A;Title: Structural evidence that endothelial cell growth factor beta is the precursor c
A;Reference number: A94127; MUID:87016918; PMID:3532107
A;Accession: B25043
A:Molecule type: protein
A;Residues: 2-155 <BUR>
A;Note: this form was designated beta endothelial cell growth factor
A;Accession: C25043
A:Molecule type: protein
A;Residues: 16-155 <BU2>
A;Note: this form was designated acidic fibroblast growth factor
A;Accession: A25043
A:Molecule type: protein
A;Residues: 22-155 <BU3>
A;Note: this form was designated alpha endothelial cell growth factor
R;Strydom, D.J.; Harper, J.W.; Lobb, R.R.
Biochemistry 25, 945-951, 1986
A;Title: Amino acid sequence of bovine brain derived class 1 heparin-binding growth fact
A;Reference number: A24539; MUID:86187766; PMID:2421762
A;Accession: A24539
A:Molecule type: protein
A;Residues: 16-155 <STR>
R;Thomas, K.A.; Gimenez-Gallego, G.; Rios-Candelore, M.; DiSalvo, J.
J. Protein Chem. 6, 163-171, 1987
A;Title: Primary structure and mitogenic and angiogenic activities of brain-derived acid
A;Reference number: A60884
A;Accession: A60884
A:Molecule type: protein
A;Residues: 16-155 <THO>
R;Kuo, M.D.; Huang, S.S.; Huang, J.S.
J. Biol. Chem. 265, 16455-16463, 1990
A;Title: Acidic fibroblast growth factor receptor purified from bovine liver is a novel
A;Reference number: A37892; MUID:90375514; PMID:2168890
A;Accession: A37892
A:Molecule type: protein
A;Residues: 22-30, 'X', 32-38 <KU2>
A;Note: this form was designated brain-derived growth factor A

A;Accession: B37892
A:Molecule type: protein
A;Residues: 16-30, 'X', 32-40 <KUO>
A;Note: this sequence is an amino-terminal fragment of a form designated as brain-derived
R;Hill, C.E.; Belford, D.A.; Godovac-Zimmermann, J.; Hendry, I.A.
Brain Res. Dev. Brain Res. 63, 13-19, 1991
A;Title: Class 1 heparin binding growth factor promotes the differentiation but not the
A;Reference number: A61198; MUID:92164087; PMID:1724209
A;Accession: A61198
A:Molecule type: protein
A;Residues: 11-26, 28-50, 53-110, 'H', 112, 'NTY', 134-155 <HIL>
R;Philippe, J.M.; Renaud, F.; Desset, S.; Laurent, M.; Mallet, J.; Courtois, Y.; Edwards, Biochem. Biophys. Res. Commun. 188, 843-850, 1992
A;Title: Cloning of two different 5' untranslated exons of bovine acidic fibroblast growth
A;Reference number: I46024; MUID:93075172; PMID:1280126
A;Accession: I46024
A;Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A;Residues: 1-18 <PH2>
A;Cross-references: EMBL:X66446; NID:g411; PIDN:CAA47063.1; PID:g412
R;Sasaki, H.; Hoshi, H.; Hong, Y.M.; Suzuki, T.; Kato, T.; Sasaki, H.; Saito, M.; Youki, J. Biol. Chem. 264, 17606-17612, 1989
A;Title: Purification of acidic fibroblast growth factor from bovine heart and its local
A;Reference number: A34477; MUID:90008933; PMID:2677012
A;Accession: A34477
A;Status: preliminary
A:Molecule type: protein
A;Residues: 16-24; 121-127; 134-143 <SAS>
A;Experimental source: heart
C;Comment: The acidic and basic fibroblast growth factors are the major endothelial-cell
ell types in vitro (although bFGF is 30-100 times more potent than aFGF in stimulating t
f these two growth factors.
C;Comment: This protein binds heparin, although less strongly than does bFGF.
C;Comment: There are some sequence similarities between residues 117-126 (a region flank
sides 18-27) and bovine substance P beta (residues 98-107).
C;Genetics:
A;Gene: HBGF-1
A;Introns: 57/1; 91/3
C;Superfamily: fibroblast growth factor
C;Keywords: acetylated amino end; angiogenesis; growth factor; heparin binding; mitogen
F;2-155/Product: beta endothelial cell growth factor #status experimental <ECB>
F;16-155/Product: acidic fibroblast growth factor #status experimental <MAT>
F;22-155/Product: alpha endothelial cell growth factor #status experimental <SCA>
F;24-28, 113-116/Region: heparin binding #status predicted
F;2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
Query Match 91.5%; Score 697; DB 1; Length 155;
Best Local Similarity 92.1%; Pred. No. 2.2e-59;
Matches 129; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
Qy 2 FNLPNGYKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHILQLSAESVGEVYIKSTE 61
Db 16 FNPLGNYKPKLLYCSNGGYFRLPDGTVGTRSDQHILQLCAESIGEVIKSTE 75
Qy 62 TGOYLAAMDTPGLYGSQTPNEECFLERLENHYNTYISKHAPKNWFVGLKKNCSCKRG 121
Db 76 TGOFLAMDTDGLLYGSQTPNEECFLERLENHYNTYISKHAEKHWFVGLKKNGRSKLG 135
Qy 122 PRHYGQKAILFLPLPVSSD 141
Db 136 PRTHFGQKAILFLPLPVSSD 155
RESULT 7
JW0055
acidic fibroblast growth factor 1 precursor - sheep
N;Alternate names: FGF-1
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 17-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004
C;Accession: JW0055
R;Grieb, T.W.; Ring, M.; Brown, E.; Palmer, C.; Belle, N.; Donjerkovic, D.; Chang, H.; Yi Biochem. Biophys. Res. Commun. 246, 182-191, 1998
A;Title: Primary structure of ovine fibroblast growth factor-1 deduced by protein and cDN

A:Reference number: JW0055; MUID:98262939; PMID:9600090
A:Accession: JW0055
A:Molecule type: mRNA
A:Residues: 1-155 <GRI>
A:Cross-references: UNIPROT:Q7M303
C:Comment: This protein is a potent mitogenic factor for NIH 3T3 fibroblasts in the absence of growth factor
C:Superfamily: fibroblast growth factor

Query Match 90.4%; Score 689; DB 2; Length 155;
Best Local Similarity 90.7%; Pred. No. 1.3e-58;
Matches 127; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 2 FNLPGNKKPKLLYCSNGGHFLRLPDGTVGDRDRSDQHIQLQLSAESVGEVYIKSTE 61
DB 16 FNLPLGNKKPKLLYCSNGGHFLRLPDGTVGDRDRSDQHIQLQLSAESVGEVYIKSTE 75

QY 62 TQOYLAMDTGLLYGSTPNEBCLFLERLEENHYNTYISKHAEKNWFVGLKKGSCKRG 121
DB 76 TQOFLAMDTGLLYGSTPNEBCLFLERLEENHYNTYISKHAEKNWFVGLKKGSCKRG 135

QY 122 PRTHYGQKAILFLPLPVSSD 141
DB 136 PRTHYGQKAILFLPLPVSSD 155

RESULT 8

Ae0130
acidic fibroblast growth factor - chicken
N:Alternate names: endothelial cell growth factor
C:Species: Gallus gallus (chicken)
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
C:Accession: Ae0130; S02639
R:Schnuerch, H.; Risau, W.
Development 111, 1143-1154, 1991
A:Title: Differentiating and mature neurons express the acidic fibroblast growth factor
A:Reference number: Ae0130; MUID:91347925; PMID:1715259
A:Accession: Ae0130
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-155 <SCH>
A:Cross-references: UNIPROT:P19596; GB:S63263; NID:G234372; PIDN:AA819629.1; PID:G234373
R:Risau, W.; Gautschi-Sova, P.; Boehlen, P.
EMBO J. 7, 959-962, 1988
A:Title: Endothelial cell growth factors in embryonic and adult chick brain are related
A:Reference number: S02639; MUID:88296438; PMID:3402441
A:Accession: S02639
A:Molecule type: protein
A:Residues: 22-30,'X',32-44,'X',46-48 <RIS>
C:Superfamily: fibroblast growth factor
C:Keywords: growth factor

Query Match 89.0%; Score 678; DB 2; Length 155;
Best Local Similarity 90.0%; Pred. No. 1.5e-57;
Matches 126; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 2 FNLPGNKKPKLLYCSNGGHFLRLPDGTVGDRDRSDQHIQLQLSAESVGEVYIKSTE 61
DB 16 FGLPLGNKKPKLLYCSNGGHFLRLPDGTVGDRDRSDQHIQLQLSAEDVGEVYIKSTA 75

QY 62 TQOYLAMDTGLLYGSTPNEBCLFLERLEENHYNTYISKHAEKNWFVGLKKGSCKRG 121
DB 76 SQOYLAMDTGLLYGSTPNEBCLFLERLEENHYNTYISKHAEKNWFVGLKKGSCKRG 135

QY 122 PRTHYGQKAILFLPLPVSSD 141
DB 136 PRTHYGQKAILFLPLPVSSD 155

RESULT 9

S00185
basic fibroblast growth factor - sheep
N:Alternate names: prostatripin
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S00185
R:Simpson, R.J.; Moritz, R.L.; Lloyd, C.J.; Fabri, L.J.; Nice, E.C.; Rubira, M.R.; Burger
FEBS Lett. 224, 128-132, 1987
A:Title: Primary structure of ovine pituitary basic fibroblast growth factor.
A:Reference number: S00185; MUID:88055577; PMID:3678486
A:Accession: S00185
A:Molecule type: protein
A:Residues: 1-146 <SIM>
C:Superfamily: fibroblast growth factor
C:Keywords: growth factor; heparin binding; mitogen
F:18-22/Region: heparin binding #status predicted
F:107-110/Region: heparin binding #status predicted

Query Match 51.8%; Score 395; DB 1; Length 146;
Best Local Similarity 56.6%; Pred. No. 1.5e-30;
Matches 77; Conservative 17; Mismatches 40; Indels 2; Gaps 1;

QY 5 PPGNVKPKLLYCSNGGHFLRLPDGTVGDRDRSDQHIQLQLSAESVGEVYIKSTETGQ 64
DB 13 PPGHFKDPKRLYCKNGGFFLRHPDGRVDGVREKSDPHIKLQQAEEGVVSIKGVCANR 72

QY 65 YLAMDTGLLYGSTPNEBCLFLERLEENHYNTYISKHAEKNWFVGLKKGSCKRGPRPT 124
DB 73 YLAMKEDGRLLASKCVTDCEFFERLESNNYNTYRSKYS--SWYVALKRTGQYKLGPKT 130

QY 125 HYGOKAILFLPLPVSS 140
DB 131 GPGOKAILFLPMSAKS 146

RESULT 10

GRBOB
basic fibroblast growth factor precursor - bovine (fragment)
N:Alternate names: bFGF; kidney-derived growth factor; prostatripin
C:Species: Bos primigenius taurus (cattle)
C:Date: 13-Aug-1986 #sequence_revision 02-Jun-1995 #text_change 09-Jul-2004
C:Accession: A24663; A32878; A33784; A61550; A61551; A60310; A61094; A01386; A60316; A222
R:Abraham, J.A.; Mergia, A.; Whang, J.L.; Tumolo, A.; Friedman, J.; Hjerrild, K.A.; Gospo
Science 233, 545-548, 1986
A:Title: Nucleotide sequence of a bovine clone encoding the angiogenic protein, basic fib
A:Reference number: A94290; MUID:86261806; PMID:2425435
A:Accession: A24663
A:Molecule type: mRNA
A:Residues: 3-157 <ABR>
A:Cross-references: UNIPROT:P03969; GB:M13440; NID:g163049; PIDN:AAA30518.1; PID:g163050
R:Experimental source: pituitary gland
R:Abraham, J.A.; Whang, J.L.; Tumolo, A.; Mergia, A.; Fiddes, J.C.
Cold Spring Harb. Symp. Quant. Biol. 51, 657-668, 1986
A:Title: Human basic fibroblast growth factor: nucleotide sequence, genomic organization,
A:Reference number: A90924; MUID:87217066; PMID:3472745
A:Accession: A32878
A:Molecule type: mRNA
A:Residues: 3-157 <AB2>
R:Minner, P.G.; Li, Y.S.; Hoffman, R.M.; Kodner, C.M.; Siegel, N.R.; Deuel, T.F.
Biochem. Biophys. Res. Commun. 165, 1096-1103, 1989
A:Title: A novel 17 kd heparin-binding growth factor (HBGF-8) in bovine uterus: purificat
A:Reference number: A33784; MUID:90121211; PMID:2610682
A:Accession: A33784
A:Molecule type: protein
A:Residues: 1-14 <MIL>
A:Note: demonstration of a possible alternative initiator or splice junction
R:Bertolini, J.; Hearn, M.T.W.
Mol. Cell. Endocrinol. 51, 187-199, 1987
A:Title: Isolation, characterization and tissue localisation of an N-terminal-truncated v
A:Reference number: A61550; MUID:87247652; PMID:3596000
A:Accession: A61550
A:Molecule type: protein
A:Residues: 16-35 <BER>
R:Ueno, N.; Baird, A.; Esch, F.; Ling, N.; Guillemin, R.
Mol. Cell. Endocrinol. 49, 189-194, 1987
A:Title: Isolation and partial characterization of basic fibroblast growth factor from bo
A:Reference number: A61551; MUID:87162856; PMID:3556754

A:Accession: A61551
A:Molecule type: protein
A:Residues: 27-35,'X',37-41 <UE3>
A:Experimental source: testes
A:Note: this form appears to be identical to the renal form
R:Ueno, N.; Baird, A.; Esch, F.; Shimazaki, S.; Ling, N.; Guillemin, R.
Regul. Pept. 16, 135-145, 1986
A:Title: Purification and partial characterization of a mitogenic factor from bovine liver
A:Reference number: A60310; MUID:87119165; PMID:3809608
A:Accession: A60310
A:Molecule type: protein
A:Residues: 23-35,'X',37-42 <UEN>
A:Experimental source: liver
R:Ueno, N.; Baird, A.; Esch, F.; Ling, N.; Guillemin, R.
Biochem. Biophys. Res. Commun. 138, 580-588, 1986
A:Title: Isolation of an amino terminal extended form of basic fibroblast growth factor.
A:Reference number: A24819; MUID:86295737; PMID:3741423
A:Contents: annotation
A:Note: the amino end of this form was blocked; the peptide composition matched what was
R:Gospodarowicz, D.; Baird, A.; Cheng, J.; Lui, G.M.; Esch, F.; Bohlen, P.
Endocrinology 118, 82-90, 1986
A:Title: Isolation of fibroblast growth factor from bovine adrenal gland: physicochemical
A:Reference number: A61094; MUID:86081530; PMID:3940857
A:Accession: A61094
A:Molecule type: protein
A:Residues: 12-25,27-35,'X',37-40 <GOS>
A:Experimental source: adrenal gland
R:Esch, F.; Baird, A.; Ling, N.; Ueno, N.; Hill, F.; Denoroy, L.; Klepper, R.; Gospodarowicz, D.
Proc. Natl. Acad. Sci. U.S.A. 82, 6507-6511, 1985
A:Title: Primary structure of bovine pituitary basic fibroblast growth factor (FGF) and
A:Reference number: A01386; MUID:86016731; PMID:3863109
A:Accession: A01386
A:Molecule type: protein
A:Residues: 12-157 <ESC>
A:Experimental source: pituitary gland
R:Baird, A.; Esch, F.; Boehlen, P.; Ling, N.; Gospodarowicz, D.
Regul. Pept. 12, 201-213, 1985
A:Title: Isolation and partial characterization of an endothelial cell growth factor from
A:Reference number: A60316; MUID:86095426; PMID:4081126
A:Accession: A60316
A:Molecule type: protein
A:Residues: 27-35,'X',37-43 <BAI>
A:Experimental source: kidney
R:Bohlen, P.; Baird, A.; Esch, F.; Ling, N.; Gospodarowicz, D.
Proc. Natl. Acad. Sci. U.S.A. 81, 5364-5368, 1984
A:Title: Isolation and partial molecular characterization of pituitary fibroblast growth
A:Reference number: A22054; MUID:84298139; PMID:6591194
A:Accession: A22054
A:Molecule type: protein
A:Residues: 12-26 <BOH>
A:Comment: The acidic and basic fibroblast growth factors are the major endothelial-cell
cell types in vitro (although bFGF is 30-100 times more potent than aFGF in stimulating b
C:Comment: This protein binds heparin more strongly than does aFGF.
C:Superfamily: fibroblast growth factor
F:1-157/Product: basic fibroblast growth factor, uterine form #status predicted <MAT1>
F:4-157/Product: basic fibroblast growth factor, pituitary gamma form #status experiment
F:12-157/Product: basic fibroblast growth factor, pituitary alpha form #status experiment
F:16-157/Product: basic fibroblast growth factor, pituitary short form #status predicted
F:23-157/Product: basic fibroblast growth factor, hepatic form #status experimental <MAT
F:27-157/Product: basic fibroblast growth factor, renal form #status experimental <MAT6>
F:29-33,118-121/Region: heparin binding #status predicted
F:4/Modified site: blocked amino end (Ala) (in mature form pituitary gamma) (probably ac

Query Match 51.8%; Score 395; DB 1; Length 157;
Best Local Similarity 56.6%; Pred. No. 1.6e-30;
Matches 77; Conservative 17; Mismatches 40; Indels 2; Gaps 1;
Oy 5 PPGNYKKPLLYCSNGGHFLRLPDGTVGTRDRSDHQLQLSAESVGEVYIKSTGTGQ 64
Db 24 PPGHFKDPKRLYCKNGGFFLRHPDGRVDGRVREKSDPHIKLQQAERGVSIVKGVANR 83
Oy 65 YLAMDTDGLLYGSGTPNECLFLERLEENHYNTYISKHAEKNWFVGLKNGSKCKRGPR 124

Db 84 YLAMKEDGRLLASCKVTDCEFFERLESNNYNTYRSKYIS--SWYVALKRTGYKLGPKT 141
Oy 125 HYGOKAILFLPLPVSS 140
Db 142 GPGQKAILFLPMSAKS 157
RESULT 11
A48834
basic fibroblast growth factor - chicken
C:Species: Gallus gallus (chicken)
C>Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A48834; S23636
R:Boerja, A.Z.; Meijers, C.; Zeller, R.
Dev. Biol. 157, 110-118, 1993
A:Title: Expression of alternatively spliced bFGF first coding exons and antisense mRNAs
A:Reference number: A48834; MUID:93246053; PMID:7683281
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-189 <BOR>
A:Cross-references: UNIPROT:Q07659
A:Experimental source: embryo
A:Note: sequence extracted from NCBI backbone (NCBIN:131000, NCBIPI:131001)
R:Mittrani, E.; Gruenbaum, Y.; Shohat, H.; Ziv, T.
Development 109, 387-393, 1990
A:Title: Fibroblast growth factor during mesoderm induction in the early chick embryo.
A:Reference number: S23636; MUID:90382254; PMID:2401202
A:Accession: S23636
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 95-128 <MIT>
A:Cross-references: EMBL:X56804; NID:g62855; PIDN:CAA40139.1; PID:g62856
C:Superfamily: fibroblast growth factor
Query Match 51.7%; Score 394; DB 2; Length 189;
Best Local Similarity 55.9%; Pred. No. 2.5e-30;
Matches 76; Conservative 17; Mismatches 41; Indels 2; Gaps 1;
Oy 5 PPGNYKKPLLYCSNGGHFLRLPDGTVGTRDRSDHQLQLSAESVGEVYIKSTGTGQ 64
Db 56 PPGHFKDPKRLYCKNGGFFLRHPDGRVDGRVREKSDPHIKLQQAERGVSIVKGSANR 115
Oy 65 YLAMDTDGLLYGSGTPNECLFLERLEENHYNTYISKHAEKNWFVGLKNGSKCKRGPR 124
Db 116 FLANKEDGRLLALKCATECEFFERLESNNYNTYRSKYSD--WYVALKRTGYKLGPKT 173
Oy 125 HYGOKAILFLPLPVSS 140
Db 174 GPGQKAILFLPMSAKS 189
RESULT 12
C37360
basic fibroblast growth factor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: C37360
R:Hebert, J.M.; Basilico, C.; Goldfarb, M.; Haub, O.; Martin, G.R.
Dev. Biol. 138, 454-463, 1990
A:Title: Isolation of cDNAs encoding four mouse FGF family members and characterization
A:Reference number: A37360; MUID:90201563; PMID:2318343
A:Accession: C37360
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-154 <HEB>
A:Cross-references: UNIPROT:P15655; GB:M30644; NID:g193296; PIDN:AAA37621.1; PID:g309239
C:Superfamily: fibroblast growth factor
Query Match 51.0%; Score 389; DB 2; Length 154;
Best Local Similarity 55.9%; Pred. No. 6e-30;
Matches 76; Conservative 17; Mismatches 41; Indels 2; Gaps 1;


```

Db      137 YLAKMEDGRLLASKCVTDCEFFERLESNNYNTYRSRKYT--SWYVALKRTGQYKLGSKT 194
Qy      125 HYGQKAILFLPLPVSS 140
          |||||:|
Db      195 GPGQKAILFLPMSAKS 210

RESULT 15
S31622
basic fibroblast growth factor - short-tailed opossum (Monodelphis domestica) (fragment)
C;Species: Monodelphis domestica
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995
C;Accession: S31622
R;Kusewitt, D.F.; Sabourin, C.L.K.; Budge, C.L.; Ley, R.D.
submitted to the EMBL Data Library, September 1992
A;Description: Characterization of cDNA encoding basic fibroblast growth factor of the m
A;Reference number: S31622
A;Accession: S31622
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-164 <KUS>
A;Cross-references: EMBL:Z15154
C;Superfamily: fibroblast growth factor

Query Match          49.9%; Score 380; DB 2; Length 164;
Best Local Similarity 55.9%; Pred. No. 4.7e-29;
Matches 76; Conservative 16; Mismatches 42; Indels 2; Gaps 1;

Qy      5 PPGNYKKPLLYCSNGGHLRILPDGTVDGTRDRSDQHTQLQLSAESVGEVYIKSTETQ 64
          |||:| || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db      31 PPGHFKDPKRLYCKNGGFFLRHPDGRVDGIREKSDPNIKLQQAERGVWSIKGVCANR 90
          ||| ||| ||| :
Qy      65 YLAMDTDGLLYGSGOTNEECLEFLERLEENHYNTYISKHAENKWFVGLKKGSCRGPR 124
          ||| ||| ||| :
Db      91 YLAKMEDGRLLALKYVTECEFFERLESNNYNTYRSRKY--NWYVALKRTGQYKLGSKT 148
          ||| ||| ||| :

Qy      125 HYGQKAILFLPLPVSS 140
          |||||:|
Db      149 GPGQKAILFLPMSAKS 164

Search completed: June 6, 2005, 07:46:22
Job time : 23.8649 secs

```

Search completed: June 6, 2005, 07:46:22
Job time : 23.8649 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 6, 2005, 07:37:37 ; Search time 107.179 Seconds
(without alignment)
673.669 Million cell updates/sec

Title: US-10-649-480A-7

Perfect score: 762

Sequence: 1 MFNLPNGYKPKLLYCSNG.....PRTHYGQXAILFLPLPVSSD 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	757	99.3	155	1	FGF1_HUMAN	P05230 homo sapien
2	744	97.6	155	1	FGF1_MESAU	P34004 mesocricetu
3	730	95.8	155	1	FGF1_MOUSE	P61148 mus musculus
4	730	95.8	155	1	FGF1_RAT	P61149 rattus norv
5	727	95.4	152	1	FGF1_PIG	P20002 sus scrofa
6	697	91.5	155	1	FGF1_BOVIN	P03968 bos taurus
7	689	90.4	155	1	FGF1_SHEEP	Q7m303 ovis aries
8	678	89.0	155	1	FGF1_CHICK	P19596 gallus gall
9	612	80.3	148	1	FGF1_CYNPY	Q616m7 cynops pyr
10	579	76.0	155	1	FGF1_XENLA	Q6glr6 xenopus lae
11	571	74.9	132	1	FGF1_NOTVI	Q7sif8 notophthalm
12	529	69.4	106	1	FGF1_CAPCA	Q9n1s8 capreolus c
13	395	51.8	154	2	Q7ZZK5	P07225 brachydanio
14	395	51.8	155	1	FGF2_BOVIN	P03969 bos taurus
15	395	51.8	155	1	FGF2_SHEEP	P20003 ovis aries
16	394	51.7	158	1	FGF2_CHICK	P48800 gallus gall
17	389	51.0	154	1	FGF2_MOUSE	P15655 mus musculus
18	389	51.0	154	1	FGF2_RAT	P13109 rattus norv
19	389	51.0	155	2	Q8QFR9	Q8qfr9 fugu rubrip
20	386	50.7	155	1	FGF2_HUMAN	P09038 homo sapien
21	386	50.7	196	2	P78443	P78443 homo sapien
22	386	50.7	210	2	Q7KZ72	Q7kz72 homo sapien
23	380	49.9	156	1	FGF2_MONDO	P48798 monodelphis
24	377.5	49.5	153	2	Q925A3	Q925a3 mus musculus
25	373	49.0	130	2	O77767	O77767 canis faml
26	370	48.6	147	1	FGF1_BRARE	Q6pbt8 brachydanio
27	364	47.8	155	1	FGF2_XENLA	P12226 xenopus lae
28	364	47.8	155	2	Q90Y92	Q90y92 cynops pyr
29	361	47.4	137	1	FGF2_RABIT	P48799 oryctolagus
30	353	46.3	64	2	Q6LBM3	Q6lbm3 homo sapien
31	348	45.7	64	2	Q7IUP6	Q7iup6 mus musculus

32	341	44.8	170	1	FGF2_CAVPO	Q60487 cavia porce
33	327	42.9	125	2	Q88TD8	Q88td8 cynops pyr
34	324	42.5	62	2	Q8SPL2	Q8spl2 equus caball
35	298	39.1	108	2	Q9N1S7	Q9n1s7 capreolus c
36	293	38.5	111	2	Q9BDX1	Q9bdx1 macaca mula
37	275	36.1	101	2	P79706	P79706 cynops pyr
38	271	35.6	96	2	Q7YRNS	Q7yrns sus scrofa
39	270	35.4	105	2	Q7TPG9	Q7tpg9 mus musculus
40	258	33.9	146	2	Q076S9	Q076s9 gallus gall
41	255	33.5	211	2	Q8C7A8	Q8c7a8 mus musculus
42	253	33.2	212	2	Q9ESL9	Q9esl9 mus musculus
43	251.5	33.0	209	1	FGF9_XENLA	Q91875 xenopus lae
44	251	32.9	211	1	FGFK_HUMAN	Q9np95 homo sapien
45	250	32.8	212	2	Q9EST9	Q9est9 rattus norv

ALIGNMENTS

RESULT 1
FGF1_HUMAN
ID FGF1_HUMAN STANDARD; PRT; 155 AA.
AC P05230; P07502;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Heparin-binding growth factor 1 precursor (HBGF-1) (Acidic fibroblast
DE growth factor) (aFGF) (Beta-endothelial cell growth factor) (ECGF-
DE beta).
GN Name=FGF1; Synonyms=FGFA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86261805; PubMed=3523756;
RA Jaye M., Howk R., Burgess W., Ricca G.A., Chiu I.-M., Ravera M.W.,
RA O'Brien S.J., Modi W.S., Maciag T., Drohan W.N.;
RT "Human endothelial cell growth factor: cloning, nucleotide sequence,
RT and chromosome localization.";
RL Science 233:541-545(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain stem;
RC MEDLINE=89343957; PubMed=2474753;
RA Wang W.P., Lehtoma K., Varban M.L., Krishnan I., Chiu I.M.;
RT "Cloning of the gene coding for human class 1 heparin-binding growth
RT factor and its expression in fetal tissues.";
RL Mol. Cell. Biol. 9:2387-2395(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain stem;
RC MEDLINE=90265618; PubMed=1693186;
RA Chiu I.-M., Wang W.P., Lehtoma K.;
RT "Alternative splicing generates two forms of mRNA coding for human
RT heparin-binding growth factor 1.";
RL Oncogene 5:755-762(1990).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=90073637; PubMed=2590193;
RA Merz A., Tischer E., Graves D., Tumolo A., Miller J.,
RA Gospodarowicz D., Abraham J.A., Shipley G.D., Fiddes J.C.;
RT "Structural analysis of the gene for human acidic fibroblast growth
RT factor.";
RL Biochem. Biophys. Res. Commun. 164:1121-1129(1989).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=92019819; PubMed=1717925;
RA Wang W.P., Quick D., Balcerzak S.P., Needleman S.W., Chiu I.M.;
RT "Cloning and sequence analysis of the human acidic fibroblast growth
RT factor gene and its preservation in leukemia patients.";
RL Oncogene 6:1521-1529(1991).

RL RP RQ
SEQUENCE FROM N.A.
MEDLINE=92202857; PubMed=1372643;
Li Y.L., Kha H., Golden J.A., Migchielsen A.A.J., Goetzl E.J.,
Turck E.J.;
"An acidic fibroblast growth factor protein generated by alternate
splicing acts like an antagonist.";
J. Exp. Med. 175:1073-1080(1992).
[7]
SEQUENCE FROM N.A.
TISSUE=Liver;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalls D.B.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[8]
SEQUENCE OF 1-154 FROM N.A.
MEDLINE=94069734; PubMed=7504343;
Zhao X.W., Yeoh T.K., Hiebert M., Frist W.H., Miller G.G.;
"The expression of acidic fibroblast growth factor (heparin-binding
growth factor-1) and cytokine genes in human cardiac allografts and T
cells.";
Transplantation 56:1177-1182(1993).
[9]
SEQUENCE OF 1-40 FROM N.A.
MEDLINE=90365758; PubMed=2393407;
Crumley G., Dionne C.A., Jaye M.;
"The gene for human acidic fibroblast growth factor encodes two
upstream exons alternatively spliced to the first coding exon.";
Biochem. Biophys. Res. Commun. 171:7-13(1990).
[10]
SEQUENCE OF 16-155.
MEDLINE=86296647; PubMed=2427112;
Harper J.W., Strydom D.J., Lobb R.R.;
"Human class I heparin-binding growth factor: structure and homology
to bovine acidic brain fibroblast growth factor.";
Biochem. Biophys. Res. Commun. 171:7-13(1990).
[11]
SEQUENCE OF 16-155.
MEDLINE=86295741; PubMed=3527167;
Gimenez-Gallego G., Conn G., Hatcher V.B., Thomas K.A.;
"The complete amino acid sequence of human brain-derived acidic
fibroblast growth factor.";
Biochem. Biophys. Res. Commun. 139:611-617(1986).
[12]
SEQUENCE OF 16-155.
MEDLINE=87048871; PubMed=3778488;
Gautschi-Sova P., Mueller T., Boehlen P.;
"Amino acid sequence of human acidic fibroblast growth factor.";
Biochem. Biophys. Res. Commun. 140:874-880(1986).
[13]
SEQUENCE OF 16-47.
MEDLINE=86186784; PubMed=3964259;
Gimenez-Gallego G., Conn G., Hatcher V.B., Thomas K.A.;
"Human brain-derived acidic and basic fibroblast growth factors: amino
terminal sequences and specific mitogenic activities.";

RL RP RQ
Biochem. Biophys. Res. Commun. 135:541-548(1986).
[14]
SEQUENCE OF 16-49.
MEDLINE=86275260; PubMed=3732516; DOI=10.1016/0014-5793(86)80812-2;
Gautschi P., Frater-Schroeder M., Boehlen P.;
"Partial molecular characterization of endothelial cell mitogens from
human brain: acidic and basic fibroblast growth factors.";
FEBS Lett. 204:203-207(1986).
[15]
X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE=96194129; PubMed=8652550; DOI=10.1021/bi9521755;
Blaber M., Disalvo J., Thomas K.A.;
"X-ray crystal structure of human acidic fibroblast growth factor.";
Biochemistry 35:2086-2094(1996).
[16]
STRUCTURE BY NMR OF 24-155.
MEDLINE=94335885; PubMed=7521397;
Pineda-Lucena A., Jimenez M.A., Nieto J.L., Santoro J., Rico M.,
Gimenez-Gallego G.;
"1H-NMR assignment and solution structure of human acidic fibroblast
growth factor activated by inositol hexasulfate.";
J. Mol. Biol. 242:81-98(1994).
[17]
STRUCTURE BY NMR OF 24-155.
MEDLINE=97107533; PubMed=8950275; DOI=10.1006/jmbi.1996.0631;
Pineda-Lucena A., Jimenez M.A., Lozano R.M., Nieto J.L., Santoro J.,
Rico M., Gimenez-Gallego G.;
"Three-dimensional structure of acidic fibroblast growth factor in
solution: effects of binding to a heparin functional analog.";
J. Mol. Biol. 284:162-178(1996).
[18]
STRUCTURE BY NMR OF 25-155.
MEDLINE=9837896; PubMed=9719643; DOI=10.1006/jmbi.1998.1977;
Lozano R.M., Jimenez M., Santoro J., Rico M., Gimenez-Gallego G.;
"Solution structure of acidic fibroblast growth factor bound to 1,3-
6-naphthalenetrisulfonate: a minimal model for the anti-tumoral action
of suramin and suradistat.";
J. Mol. Biol. 281:899-915(1998).
CC CC CC
in vivo and are potent mitogens for a variety of cell types in
vitro. There are differences in the tissue distribution and
concentration of these 2 growth factors.
CC CC CC
-1- SUBUNIT: Monomer.
CC CC CC
-1- MISCELLANEOUS: This protein binds heparin, although less strongly
than does bFGF.
CC CC CC
-1- SIMILARITY: Belongs to the heparin-binding growth factors family.
CC CC CC
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.iesb-sib.ch/announce/>
or send an email to license@sib-sib.ch).
CC CC CC
EMBL; M13361; AAA79245.1; -
DR EMBL; X51943; CAA36206.1; -
DR EMBL; M30492; AAA52446.1; -
DR EMBL; M30490; AAA52446.1; JOINED.
DR EMBL; M30491; AAA52446.1; JOINED.
DR EMBL; M60515; AAA51672.1; -
DR EMBL; M60516; AAA51673.1; -
DR EMBL; M23087; AAA52638.1; -
DR EMBL; M23086; AAA52638.1; JOINED.
DR EMBL; BC032697; AAH32697.1; -
DR EMBL; S67291; AAB29057.2; -
DR EMBL; X65778; CAA46661.1; -
DR PIR; A33665; A33665.
DR PDB; 1AXM; X-ray; A/B/C/D/E/F=21-154.
DR PDB; 1DJS; X-ray; B=21-154.
DR PDB; 1DZC; NMR; A=25-155.
DR PDB; 1DZD; NMR; A=29-155.
DR PDB; 1B00; X-ray; A/C=16-155.

DR PDB; 1EVT; X-ray; A/B=22-155.
DR PDB; 1JQZ; X-ray; A/B=10-155.

Query Match 99.3%; Score 757; DB 1; Length 155;
Best Local Similarity 100.0%; Pred. No. 7.5e-66;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FNLPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRSDRSDQHILQQLSAESVGVYIKSTE 61
DB 16 FNLPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRSDRSDQHILQQLSAESVGVYIKSTE 75

QY 62 TQOYLAMTDGLLYGSQTPNEECLFLERLEENHNYTYISKHAEKNWFVGLKKGSCCKRG 121
DB 76 TQOYLAMTDGLLYGSQTPNEECLFLERLEENHNYTYISKHAEKNWFVGLKKGSCCKRG 135

QY 122 PRTHYGQKAILFLPLPVSSD 141
DB 136 PRTHYGQKAILFLPLPVSSD 155

RESULT 2
FGF1 MESAU
ID FGF1 MESAU STANDARD; PRT; 155 AA.
AC P34004;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Heparin-binding growth factor 1 precursor (HBGF-1) (Acidic fibroblast growth factor) (aFGF).
GN Name=FGF1; Synonyms=FGF-1;
OC Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90270291; PubMed=1693366;
RA Hall J.A., Harris M.A., Malark M., Mansson P.E., Zhou H., Harris S.E.;
RT "Characterization of the hamster DDT-1 cell aFGF/HBGF-I gene and cDNA and its modulation by steroids.";
RL J. Cell. Biochem. 43:17-26(1990).
CC -!- FUNCTION: The heparin-binding growth factors are angiogenic agents in vivo and are potent mitogens for a variety of cell types in vitro. There are differences in the tissue distribution and concentration of these 2 growth factors.
CC -!- SUBUNIT: Monomer.
CC -!- MISCELLANEOUS: This protein binds heparin, although less strongly than does bFGF.
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
DR PIR; A60721; A60721.
DR HSSP; P05230; 1EVT.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR002209; HB/F growthfact.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00263; HBGF.FGF.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
KW Angiogenesis; Growth factor; Heparin-binding; Mitogen.
FT PROPEP 1 15 By similarity.
FT CHAIN 16 155 Heparin-binding growth factor 1.
FT DOMAIN 24 28 Heparin binding (Potential).
FT DOMAIN 113 116 Heparin binding (Potential).
SQ SEQUENCE 155 AA; 17403 MW; 41E5EC760B412CC5 CRC64;

Query Match 97.6%; Score 744; DB 1; Length 155;
Best Local Similarity 97.9%; Pred. No. 1.4e-64;
Matches 137; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FNLPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRSDRSDQHILQQLSAESVGVYIKSTE 61

DR PDB; 1EVT; X-ray; A/B=22-155.
DR PDB; 1JQZ; X-ray; A/B=10-155.

Query Match 99.3%; Score 757; DB 1; Length 155;
Best Local Similarity 100.0%; Pred. No. 7.5e-66;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FNLPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRSDRSDQHILQQLSAESVGVYIKSTE 61
DB 16 FNLPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRSDRSDQHILQQLSAESVGVYIKSTE 75

QY 62 TQOYLAMTDGLLYGSQTPNEECLFLERLEENHNYTYISKHAEKNWFVGLKKGSCCKRG 121
DB 76 TQOYLAMTDGLLYGSQTPNEECLFLERLEENHNYTYISKHAEKNWFVGLKKGSCCKRG 135

QY 122 PRTHYGQKAILFLPLPVSSD 141
DB 136 PRTHYGQKAILFLPLPVSSD 155

RESULT 3
FGF1 MOUSE
ID FGF1 MOUSE STANDARD; PRT; 155 AA.
AC P61148; P10935;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Heparin-binding growth factor 1 precursor (HBGF-1) (Acidic fibroblast growth factor) (aFGF).
GN Name=FGF1; Synonyms=FGF-1, Fgfa;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90201563; PubMed=2318343;
RA Hebert J.M., Basilico C., Goldfarb M., Haub O., Martin G.R.;
RT "Isolation of cDNAs encoding four mouse EGF family members and characterization of their expression patterns during embryogenesis.";
RL Dev. Biol. 138:454-463(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97128312; PubMed=8972905; DOI=10.1016/S0378-1119(96)00365-4;
RA Madiar F., Hackshaw K.V., Chiu I.M.;
RT "Cloning and characterization of the mouse Fgf-1 gene.";
RL Gene 179:231-236(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=97094746; PubMed=8939980; DOI=10.1074/jbc.271.47.30263;
RA Alam K.Y., Frostholm A., Hackshaw K.V., Evans J.E., Rotter A., Chiu I.M.;
RT "Characterization of the 1B promoter of fibroblast growth factor 1 and its expression in the adult and developing mouse brain.";
RL J. Biol. Chem. 271:30263-30271(1996).
CC -!- FUNCTION: The heparin-binding growth factors are angiogenic agents in vivo and are potent mitogens for a variety of cell types in vitro. There are differences in the tissue distribution and concentration of these 2 growth factors.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M30641; AAA37618.1; -.
DR EMBL; U36459; AAC52969.1; -.
DR EMBL; U36457; AAC52969.1; JOINED.
DR EMBL; U36458; AAC52969.1; JOINED.
DR EMBL; U67610; AAC52907.1; -.
DR PIR; D37360; D37360.
DR HSSP; P05230; 1EVT.
DR MGD; MGI:95515; Fgf1.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR002348; IL1_HBGF.


```
or send an email to license@isb-sib.ch).
-----
CC EMBL; X60317; CAA42869.1; -.
DR PIR; JH0476; JH0476.
DR HSSP; P05230; LEVT.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR02209; HB/F growthFact.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PRO0263; HBGFHGF.
DR PRINTS; PRO0262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
KW Angiogenesis; Direct protein sequencing; Growth factor;
KW Heparin-binding; Mitogen.
FT PROPEP 1 15
FT CHAIN 16 >152 Heparin-binding growth factor 1.
FT CHAIN 22 >152 Endothelial cell growth factor alpha.
FT CHAIN 24 28 Heparin binding (Potential).
FT DOMAIN 113 116 Heparin binding (Potential).
FT DOMAIN 31 39 C -> S (in Ref. 2).
FT CONFLICT 31 39 R -> Y (in Ref. 2).
FT NON TER 152 152
SQ SEQUENCE 152 AA; 17103 MW; AE853B0A92F9ABF4 CRC64;

Query Match 95.4%; Score 727; DB 1; Length 152;
Best Local Similarity 97.8%; Pred. No. 6.2e-63;
Matches 134; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FNLPPGNVKKPKLLYCSNGHFLRLPDGTGTRDSQDHIQLQLSAESVGEVYIKSTE 61
DB 16 FNLPPGNVKKPKLLYCSNGHFLRLPDGTGTRDSQDHIQLQLSAESVGEVYIKSTE 75

QY 62 TQYLAMDTGILYGSQTPNECLFLERLEENHNTYISKHAERNWVGLKNGSKRG 121
DB 76 TQYLAMDTGILYGSQTPNECLFLERLEENHNTYISKHAERNWVGLKNGSKRG 135

QY 122 PRTHYGQKAILFLPLPV 138
DB 136 PRTHYGQKAILFLPLPV 152

RESULT 6
FGF1 BOVIN STANDARD; PRT; 155 AA.
AC P03568.
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Heparin-binding growth factor 1 precursor (HBGF-1) (Acidic fibroblast
DE growth factor) (aFGF) (Prostatein) (Endothelial cell growth factor
DE beta and alpha chains) (Acidic eye-derived growth factor II) (EDGF
DE II).
GN Name=FGF1; Synonyms=AFGF, FGF-1, FGFA, HBGF-1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89083506; PubMed=3205724;
RA Halley C., Courtois Y., Laurent M.;
RT "Nucleotide sequence of bovine acidic fibroblast growth factor cDNA.";
RL Nucleic Acids Res. 16:10913-10913(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Retina;
RC MEDLINE=89078619; PubMed=2849564; DOI=10.1016/0014-5793(88)80981-5;
RA Alterio J., Halley C., Brou C., Soussi T., Courtois Y., Laurent M.;
```

```
RT "Characterization of a bovine acidic FGF cDNA clone and its expression
RL in brain and retina.";
RN FEBS Lett. 242:41-46(1988).
RP [3]
RX SEQUENCE OF 2-155.
RA MEDLINE=87016918; PubMed=3532107;
RA Burgess W.H., Mehlman T., Marshak D.R., Fraser B.A., Maciag T.;
RT "Structural evidence that endothelial cell growth factor beta is the
RT precursor of both endothelial cell growth factor alpha and acidic
RT fibroblast growth factor.";
RN Proc. Natl. Acad. Sci. U.S.A. 83:7216-7220(1986).
RL [4]
RX SEQUENCE OF 2-155.
RA MEDLINE=87026586; PubMed=3768327;
RA Crabb J.W., Ames L.G., Carr S.A., Johnson C.M., Roberts G.D.;
RT "Complete primary structure of prostatein, a prostate epithelial
RT cell growth factor.";
RL Biochemistry 25:4988-4993(1986).
RN [5]
RX SEQUENCE OF 16-155.
RA MEDLINE=86070224; PubMed=4071057;
RA Gineez-Gallego G., Rodkey J., Bennett C., Rios-Candelore M.;
RA Disalvo J., Thomas K.;
RT "Brain-derived acidic fibroblast growth factor: complete amino acid
RT sequence and homologies.";
RL Science 230:1385-1388(1985).
RN [6]
RX SEQUENCE OF 16-44, AND AMINO-ACID COMPOSITION.
RA MEDLINE=86055750; PubMed=4065099;
RA Boehlen P., Each P., Baird A., Gospodarowicz D.;
RT "Acidic fibroblast growth factor (FGF) from bovine brain: amino-
RT terminal sequence and comparison with basic FGF.";
RL EMBO J. 4:1951-1956(1985).
RN [7]
RX SEQUENCE OF 16-56 FROM N.A.
RA MEDLINE=86261806; PubMed=2425435;
RA Abraham J.A., Mergia A., Whang J.L., Tumolo A., Friedman J.,
RA Hjerild K.A., Gospodarowicz D., Fiddes J.C.;
RT "Nucleotide sequence of a bovine clone encoding the angiogenic
RT protein, basic fibroblast growth factor.";
RL Science 233:545-548(1986).
RN [8]
RX SEQUENCE OF 16-45.
RA MEDLINE=89231704; PubMed=2714282;
RA Quinkler W., Maasberg M., Bernotat-Danielowski S., Luethke N.,
RA Sharma H.S., Schaper W.;
RT "Isolation of heparin-binding growth factors from bovine, porcine and
RT canine hearts.";
RL Eur. J. Biochem. 181:67-73(1989).
RN [9]
RX SEQUENCE OF 1-18 FROM N.A.
RA Philippe J.M., Renaud F., Desset S., Laurent M.;
RL Submitted (JUL-1992) to the EMBL/GenBank/DBJ databases.
RN [10]
RX X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RA MEDLINE=91095983; PubMed=1702556;
RA Zhu X., Komiya H., Chirino A., Faham S., Fox G.M., Arakawa T.,
RA Hsu B.T., Rees D.C.;
RT "Three-dimensional structures of acidic and basic fibroblast growth
RT factors.";
RL Science 251:90-93(1991).
CC -1- FUNCTION: The heparin-binding growth factors are angiogenic agents
CC in vivo and are potent mitogens for a variety of cell types in
CC vitro. There are differences in the tissue distribution and
CC concentration of these 2 growth factors.
CC -1- SUBUNIT: Monomer.
CC -1- MISCELLANEOUS: This protein binds heparin, although less strongly
CC than does bFGF.
CC -1- SIMILARITY: Belongs to the heparin-binding growth factors family.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
```

the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; M13439; AAA30516.1; -
CC EMBL; X13221; CRA31610.1; -
CC EMBL; X14032; CRA32192.1; -
CC EMBL; M35608; AAA30517.1; -
CC EMBL; X66446; CRA47063.1; -
CC EMBL; M97660; AAA30563.1; -
CC EMBL; M97661; AAA30564.1; -
CC PIR; JH0613; GKBOA.
DR PDB; 1AFC; X-ray; A/B/C/D/E/F/G/H=16-155.
DR PDB; 1BAR; X-ray; A/B=16-155.
DR InterPro; IPR008996; Cytok_IL1_like.
DR InterPro; IPR002209; HB/F growthfact.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00263; HBGF_FGF.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
DR 3D-structure; Acetylation; Angiogenesis; Direct protein sequencing;
KW Growth factor; Heparin-binding; Mitogen.
FT PROPEP 1 15
FT CHAIN 2 155 Endothelial cell growth factor beta.
FT CHAIN 16 155 Heparin-binding growth factor 1.
FT CHAIN 22 155 Endothelial cell growth factor alpha.
FT DOMAIN 24 28 Heparin binding (Potential).
FT DOMAIN 113 116 Heparin binding (Potential).
FT MOD RES 2 2 N-acetylalanine.
FT TURN 23 24
FT TURN 27 31
FT TURN 32 35
FT STRAND 36 37
FT STRAND 39 40
FT TURN 42 43
FT STRAND 45 47
FT TURN 52 53
FT TURN 56 57
FT STRAND 59 65
FT TURN 66 67
FT STRAND 68 73
FT TURN 74 76
FT STRAND 79 79
FT STRAND 82 82
FT TURN 84 85
FT STRAND 87 89
FT STRAND 91 91
FT STRAND 96 98
FT HELIX 100 104
FT TURN 106 107
FT STRAND 110 114
FT TURN 116 117
FT TURN 118 120
FT TURN 121 121
FT STRAND 123 123
FT STRAND 126 126
FT TURN 128 129
FT STRAND 131 132
FT STRAND 134 134
FT STRAND 135 137
FT TURN 140 141
FT HELIX 143 145
FT STRAND 147 151
SQ SEQUENCE 155 AA; 17493 MW; F636641F189F9BFD CRC64;
Query Match 91.5%; Score 697; DB 1; Length 155;
Best Local Similarity 92.1%; Pred. No. 5.4e-60;
Matches 129; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 2 FNLPPGNYKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESGVEYIKSTE 61
Db 16 FNLPLGNYKPKLLYCSNGGVFLRLPDGTVDGTRDRSDQHIQLQLCAESIGVEYIKSTE 75
Qy 62 TGOVLAMDTGCLLYGSQTPNEECFLERLEBNHYNTYISKHAENWVFLGKKGSCRG 121
Db 76 TGOFLAMDTGCLLYGSQTPNEECFLERLEBNHYNTYISKHAENWVFLGKKGSKLG 135
Qy 122 PRTHYGOKAILFLPLPVSSD 141
Db 136 PRTHFGOKAILFLPLPVSSD 155
RESULT 7
FGF1_SHEEP STANDARD; PRT; 155 AA.
ID _FGF1_SHEEP
AC Q7M303;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Heparin-binding growth factor 1 precursor (HBGF-1) (Acidic fibroblast growth factor) (aFGF).
GN Name=FGF1;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
OX [1]
RN SEQUENCE FROM N.A.
RP PubMed=9600090; DOI=10.1006/bbrc.1998.8597;
RX Grieb T.W., Ring M., Brown E., Palmer C., Belle N., Donjerkovic D., Chang H., Yun J., Subramanian R., Forozan F., Guo Y., Vertes A., Winkles J.A., Burgess W.H.;
RA "Primary structure of ovine fibroblast growth factor-1 deduced by protein and cDNA analysis.";
RL Biochem. Biophys. Res. Commun. 246:182-191(1998).
CC -!- FUNCTION: The heparin-binding growth factors are angiogenic agents in vivo and are potent mitogens for a variety of cell types and vitro. There are differences in the tissue distribution and concentration of these 2 growth factors (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- MISCELLANEOUS: This protein binds heparin, although less strongly than does bFGF (By similarity).
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family. PIR; JMW055; JMW055.
DR InterPro; IPR002209; HB/F growthfact.
DR InterPro; IPR002348; IL1_HBGF.
DR PRINTS; PR00263; HBGF_FGF.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
KW Angiogenesis; Growth factor; Heparin-binding; Mitogen.
FT PROPEP 1 15 By similarity.
FT CHAIN 16 155 Heparin-binding growth factor 1.
FT DOMAIN 24 28 Heparin binding (Potential).
FT DOMAIN 113 116 Heparin binding (Potential).
SQ SEQUENCE 155 AA; 17557 MW; FE7CDEC3D35008EF CRC64;
Query Match 90.4%; Score 689; DB 1; Length 155;
Best Local Similarity 90.7%; Pred. No. 3.2e-59;
Matches 127; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
Qy 2 FNLPPGNYKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESGVEYIKSTE 61
Db 16 FNLPLGNYKPKLLYCSNGGVFLRLPDGTVDGTRDRSDQHIQLQLCAESIGVEYIKSTE 75
Qy 62 TGOVLAMDTGCLLYGSQTPNEECFLERLEBNHYNTYISKHAENWVFLGKKGSCRG 121
Db 76 TGOFLAMDTGCLLYGSQTPNEECFLERLEBNHYNTYISKHAENWVFLGKKGSKLG 135
Qy 122 PRTHYGOKAILFLPLPVSSD 141


```
FT BINDING 109 112 Heparin (Potential).
FT NON TER 148
SQ SEQUENCE 148 AA; 16946 MW; C74C2200FCA37AD8 CRC64;

Query Match 80.3%; Score 612; DB 1; Length 148;
Best Local Similarity 82.5%; Pred. No. 1e-51; 14; Indels 0; Gaps 0;
Matches 113; Conservative 10; Mismatches 10;

Qy 2 FNLPPGNYKKPKLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
Db 12 FNLPGNYQRPKLYCSNGGHFLRLPDGKVDGTRDRSDPYIQLQFYAESVGEVYIKSL 71

Qy 62 TGOYLAMTDGLLYGSQTPNEECFLERLEENHNNTYISKHAEKNWFVGLKKNKSGCKRG 121
Db 72 TGOYLAMDSGRLYASQSPSEECFLERLEENHNNTYISKHAEKNWFVGLKKNKSGCKRG 131

Qy 122 PRTHYGOKAILFLPLPV 138
Db 132 SRTHFGKAILFLPLPV 148

RESULT 10
FGF1_XENLA STANDARD; PRT; 155 AA.
AC Q6GLR6;
DT 25-JAN-2005 (Rel. 46, Created)
DT 25-JAN-2005 (Rel. 46, Last sequence update)
DE Heparin-binding growth factor 1 precursor (HBGF-1) (Fibroblast growth factor 1) (FGF-1) (Acidic fibroblast growth factor) (aFGF).
GN Name=FGF1;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RG NIH - Xenopus Gene Collection (XGC) project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: The heparin-binding growth factors are angiogenic agents in vivo and are potent mitogens for a variety of cell types in vitro. There are differences in the tissue distribution and concentration of these 2 growth factors (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- MISCELLANEOUS: This protein binds heparin, although less strongly than does bFGF (By similarity).
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
-----
DR EMBL; BC074391.1; -;
DR InterPro; IPR008996; Cytok_IL1_ like.
DR InterPro; IPR002209; HB/F_Growthfact.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00263; HGGFFGF.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
KW Angiogenesis; Growth factor; Heparin-binding; Mitogen.
FT PROPEP 1 15
FT CHAIN 16 155
FT BINDING 24 28 Heparin-binding growth factor 1.
FT BINDING 113 116 Heparin (Potential).
```

```
SQ SEQUENCE 155 AA; 17318 MW; 49F5F0E465BA6597 CRC64;

Query Match 76.0%; Score 579; DB 1; Length 155;
Best Local Similarity 76.4%; Pred. No. 1.8e-48;
Matches 107; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

Qy 2 FNLPPGNYKKPKLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
Db 16 FSLPIGNYKKPKLYCNGGVFLRLPEGVVDGTRDRNDLYITLKLALSQGEVHIKTE 75

Qy 62 TGOYLAMTDGLLYGSQTPNEECFLERLEENHNNTYISKHAEKNWFVGLKKNKSGCKRG 121
Db 76 TGCYLAMDSSGQLYGTUTPNEECFLERLEENHNNTYISKYADNMNWFVGLKKNKSGCKG 135

Qy 122 PRTHYGOKAILFLPLPVSSD 141
Db 136 SRTHYGOKAILFLPLPASPD 155

RESULT 11
FGF1_NOTVI STANDARD; PRT; 132 AA.
AC Q7SI8;
DT 25-JAN-2005 (Rel. 46, Created)
DT 25-JAN-2005 (Rel. 46, Last sequence update)
DE Heparin-binding growth factor 1 (HBGF-1) (Fibroblast growth factor 1) (FGF-1) (Acidic fibroblast growth factor) (aFGF) (Fragment).
GN Name=FGF1;
OS Notoththalmus viridescens (Eastern newt) (Triturus viridescens).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
OC Notoththalmus.
OX NCBI_TaxID=8316;
RN [1]
RP STRUCTURE BY NMR.
RA Arunkumar A.I., Srisaillam S., Kumar T.K.S., Chiu I.M., Yu C.;
RL Submitted (AUG-2000) to the PDB data bank.
CC -!- FUNCTION: The heparin-binding growth factors are angiogenic agents in vivo and are potent mitogens for a variety of cell types in vitro. There are differences in the tissue distribution and concentration of these 2 growth factors (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- MISCELLANEOUS: This protein binds heparin, although less strongly than does bFGF (By similarity).
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
PDB; 1FMM; NMR; S=1-132.
DR InterPro; IPR008996; Cytok_IL1_ like.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR ProDom; PD000831; IL1_HBGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
KW 3D-structure; Angiogenesis; Growth factor; Heparin-binding; Mitogen.
FT NON TER 1 1
FT BINDING 1 5 Heparin (Potential).
FT BINDING 90 93 Heparin (Potential).
SQ SEQUENCE 132 AA; 15015 MW; 76CABAF337B29C7B CRC64;
```

```
Query Match 74.9%; Score 571; DB 1; Length 132;
Best Local Similarity 81.1%; Pred. No. 9.8e-48;
Matches 107; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

Qy 10 KKPCLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTEQYLA 69
Db 1 QKPCLLYCSNGGVFLRLFPDGKVDGTRDRSDPYIQLQFYAESVGEVYIKSLQYLA 60

Qy 70 TDGLLYGSQTPNEECFLERLEENHNNTYISKHAEKNWFVGLKKNKSGCKRGPTHYQK 129
Db 61 SDGLYASQSPSEECFLERLEENHNNTYISKVHADKDFVGIKKNKGTGSRTHFGQK 120

Qy 130 AILFLPLPVSSD 141
Db 121 AILFLPLPVSSD 132
```

```
RESULT 12
FGF1_CAPCA
ID FGF1_CAPCA STANDARD; PRT; 106 AA.
AC Q9N1S8;
DT 25-JAN-2005 (Rel. 46, Created)
DT 25-JAN-2005 (Rel. 46, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Heparin-binding growth factor 1 (HBGF-1) (Fibroblast growth factor 1)
DE (FGF-1) (Acidic fibroblast growth factor) (aFGF) (Fragment).
GN Name=FGF1;
OS Capreolus capreolus (Roe deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Odocoileinae; Capreolus.
OX NCBI_TaxID=9858;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=20532861; PubMed=11078967; DOI=10.1016/S0378-4320(00)00191-3;
RA Wagener A., Blotner S., Goritz F., Fickel J.;
RT "Detection of growth factors in the testis of roe deer (Capreolus capreolus).";
RL Anim. Reprod. Sci. 64:65-75(2000).
CC -!- FUNCTION: The heparin-binding growth factors are angiogenic agents
CC in vivo and are potent mitogens for a variety of cell types in
CC vitro. There are differences in the tissue distribution and
CC concentration of these 2 growth factors (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- MISCELLANEOUS: This protein binds heparin, although less strongly
CC than does bFGF (By similarity).
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF152586; AAF73225.1; -.
DR HSP; P05230; IJQ2.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR002209; HB/F growthfact.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00263; HBGF_FGF.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
KW Angiogenesis; Growth factor; Heparin-binding; Mitogen.
FT NON_TER 1
FT BINDING 83 86 Heparin (Potential).
FT NON_TER 106 106
SQ SEQUENCE 106 AA; 11931 MW; 2EE9C9C1D749A5023 CRC64;

Query Match 69.4%; Score 529; DB 1; Length 106;
Best Local Similarity 91.5%; Pred. No. 8.5e-44;
Matches 97; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 17 CSNGGHFLRLPDGTGDRSDQHILQLSAESVGEVYIKSTETGQYLAAMDTDGLLYG 76
DQ 1 CRNGGHFLRLPDGTGDRSDQHILQLSAESVGEVYIKSTETGQYLAAMDTDGLLYG 60

QY 77 SQTPEECFLERLEENHYNTYISKHAEKNWVGLKKNQSKRG 122
DQ 61 SQTPEECFLERLEENHYNTYISKHAEKNWVGLKKNQSKRG 106

RESULT 13

Query Match 51.8%; Score 395; DB 2; Length 154;
Best Local Similarity 56.0%; Pred. No. 1.6e-30;
Matches 75; Conservative 22; Mismatches 35; Indels 2; Gaps 1;

QY 3 NLPQNYKKPLKLYCSNGGHFLRLPDGTGDRSDQHILQLSAESVGEVYIKSTET 62
DQ 19 SPPAGSFDPKRLCYKNGGFFLRINADGRVGDGARDKSDPHIRLQLQATAVGEVLKIGCT 78

QY 63 GOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAEKNWVGLKKNQSKRG 122
DQ 79 NRFLAMNADGRLFGTKRTTDCYFLERLESNNYNTYRSRKYPD--WYVALKRTGQYKSGS 136

QY 123 RTHYGQKAILFLPL 136
DQ 137 KTSFGQKAILFLPM 150

RESULT 14
FGF2_BOVIN
ID_FGF2_BOVIN STANDARD; PRT; 155 AA.
AC P03969;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Heparin-binding growth factor 2 precursor (HBGF-2) (Basic fibroblast
DE growth factor) (BFGF) (Prostatropin) (Contains: Kidney-derived growth
DE factor).
GN Name=FGF2; Synonyms=FGF-2;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86261806; PubMed=2425435;
RA Abraham J.A., Mergia A., Whang J.L., Tumolo A., Friedman J.,
RA Hjerild K.A., Gospodarowicz D., Fiddes J.C.;
RT "Nucleotide sequence of a bovine clone encoding the angiogenic
```


OC Caprinae; Ovis.
OX NCBI_taxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RL Sutton R., Ward W.G., Raphael K.A., Cam G.R.;
RN Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 9-155.
RX MEDLINE=85055577; PubMed=3678486; DOI=10.1016/0014-5793(87)80435-0;
RA Simpson R.J., Moritz R.L., Lloyd C.J., Fabri L.J., Nice E.C.,
RA Rubira M.R., Burgess A.W.;
RT "Primary structure of ovine pituitary basic fibroblast growth
RT factor.";
RL FEBS Lett. 224:128-132(1987).
CC -!- FUNCTION: The heparin-binding growth factors are angiogenic agents
CC in vivo and are potent mitogens for a variety of cell types in
CC vitro. There are differences in the tissue distribution and
CC concentration of these 2 growth factors.
CC -!- SUBUNIT: Monomer.
CC -!- MISCELLANEOUS: This protein binds heparin more strongly than does
CC aFGF.
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L36136; AAA31519.1; -.
DR HSSP; P09038; IBFF.
DR InterPro; IPR008996; Cytok_IL1_like.
DR InterPro; IPR002209; HB/F growthfact.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00263; HBGFPGF.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
KW Angiogenesis; Direct protein sequencing; Growth factor;
KW Heparin-binding; Mitogen.
FT PROPEP 1
FT CHAIN 10 155 Heparin-binding growth factor 2.
FT DOMAIN 27 31 Heparin binding (Potential).
FT DOMAIN 116 119 Heparin binding (Potential).
FT SITE 46 48 Cell attachment site (atypical)
FT SITE 88 90 (Potential).
FT SITE 88 90 Cell attachment site (atypical)
FT (Potential).
SQ SEQUENCE 155 AA; 17280 MW; B5F2364BA610606D CRC64;

Query Match 51.8%; Score 395; DB 1; Length 155;
Best Local Similarity 56.6%; Pred. NO. 1.6e-30;
Matches 77; Conservative 17; Mismatches 40; Indels 2; Gaps 1;

QY 5 PPGNYKKPKLYCSNGHFLRILPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTGTGQ 64
DB 22 PPGHFKDPRLYCKNGGFFLIHPDGRVDGVRKSDPHIKLQQAEEGVVSIKGVCANR 81

QY 65 YLAMDTGLLYGSGTPNECLFLERLENNHYNTYISKHAENKWNFVLKKNKSGCKRGPT 124
DB 82 YLAWKEDGRLLASKCVTDCCFFERLESNNYNTYRSKYS--SWYVALKRTGYKLGPKT 139

QY 125 HYGQKAILFLPLVSS 140
DB 140 GPGQKAILFLPMSAKS 155

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 16, 2005, 22:50:01 ; Search time 475 Seconds
(without alignments)
7851.446 Million cell updates/sec

Title: US-10-649-480A-6
Perfect score: 630
Sequence: 1 ggttagagatcgagatctc.....ctgagatcggctgctaaca 630

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	630	100.0	630	6	ABK10595 cDNA enco
2	630	100.0	630	6	Aak98920 Codon opt
3	630	100.0	630	12	Ado55205 Human aci
4	584	92.7	630	6	ABK10594
5	584	92.7	630	6	Aak98919 Codon opt
6	584	92.7	630	12	Ado55203 Human aci
7	567.4	90.1	990	6	Aak98922 Codon opt
8	536	85.1	630	6	ABK10592
9	536	85.1	630	6	Aak98917
10	536	85.1	630	12	Ado55200 Human aci
11	341.6	54.2	8501	2	Ado55200 Human aci
12	290	46.0	454	2	AAQ02421 cDNA enco
13	290	46.0	454	2	AAQ03873 Synthetic
14	290	46.0	454	2	AAQ10399 Human aci
15	290	46.0	454	2	AAQ10166 Human aci
16	290	46.0	454	2	AAQ025916 afGF mute
17	288.8	45.8	496	2	AAQ03871 Synthetic
18	286.8	45.5	440	1	AAQ03871 Synthetic
19	285.4	45.3	490	11	AAQ03871 Human aci
20	285.4	45.3	638	1	AAQ03871 Human aci

21	285.4	45.3	638	1	AAQ03871 Human aci
22	285.4	45.3	638	2	AAQ03871 Human aci
23	285.4	45.3	638	2	AAQ03871 Human aci
24	285.4	45.3	638	2	AAQ03871 Human aci
25	285.4	45.3	638	9	AAQ04028 Thrombin
26	285.4	45.3	639	2	AAQ045985 Human end
27	285.4	45.3	920	10	ADL13664 Osteoarthritis
28	285.4	45.3	2259	10	ADL13660 Osteoarthritis
29	285.4	45.3	2297	13	ADT89313 Human aci
30	285.4	45.3	2357	10	ACC42968 Human FIB
31	285.4	45.3	2357	13	ADT89313 Human aci
32	285.4	45.3	3289	13	ADQ33036 Human SNP
33	285.4	45.3	3677	13	ADQ33036 Human SNP
34	285.4	45.3	4083	13	ADQ33040 Human SNP
35	285.4	45.3	4087	8	ABX63225 Human cDN
36	284	45.1	468	6	ABV78179 Human DNA
37	284	45.1	468	6	ABX35755 Human pol
38	284	45.1	468	6	ABX09998 Human DNA
39	284	45.1	468	6	Aak98918 Human aci
40	284	45.1	468	6	ABL91720 Human pol
41	284	45.1	468	10	ADL13661 Osteoarthritis
42	284	45.1	468	12	Ado55202 Human aci
43	284	45.1	468	13	ADQ94629 Human FGF
44	281.8	44.7	420	2	AAQ88233 Bovine af
45	281.6	44.7	462	2	AAQ45983 Human end

ALIGNMENTS

RESULT 1
ABK10595
ID ABK10595 standard; cDNA; 630 BP.

XX AC ABK10595;

XX 05-JUN-2002 (first entry)

XX cDNA encoding human acidic FGF protein (haFGF140).

XX haFGF140; acidic fibroblast growth factor; cell proliferation;
XX differentiation; tumorigenesis; metastasis; chromosome 5;
XX ss; human.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

XX CDS 122..529

XX FT /*tag= a

XX FT /product= "HaFGF 140 protein"

XX WO200214471-A2.

XX 21-FEB-2002.

XX 15-AUG-2001; 2001WO-US025537.

XX 15-AUG-2000; 2000US-0225406P.

XX (PHAG-) PHAGE BIOTECHNOLOGY CORP.

XX Stegmann TJ, Kordyum VA, Chernykh SI, Slavchenko IY, Vozianov OF;

XX WPI; 2002-257598/30.

XX P-PSDB; AAU76945.

XX Producing a biologically active human acidic fibroblast growth factor
XX (haFGF) protein for use in promoting angiogenesis, involves employing an
XX E. coli transformed with a plasmid having an haFGF gene operably linked
XX to a promoter.

XX Disclosure; Fig 8; 41pp; English.

XX This invention relates to a novel method for producing a biologically
CC active human acidic fibroblast growth factor (hAFGF) protein. Fibroblast
CC growth factors are potent regulators of cell proliferation, differentiation
CC and normal development and they have been shown to play a
CC role in tumorigenesis and metastasis. Acidic fibroblast growth factor
CC has been shown to be potent inducers of angiogenesis. The gene for acidic
CC fibroblast growth factor is located on human chromosome 5. The method of
CC the invention comprises employing a plasmid having at least one copy of
CC a gene, which encodes a biologically active hAFGF protein operably linked
CC to a promoter, to transform *Escherichia coli*. The method is useful for
CC producing recombinant or biologically active hAFGF protein, which is
CC useful in promoting angiogenesis. The present sequence represents a cDNA
CC encoding the human acidic fibroblast growth factor 140 protein (hAFGF140)
CC used in the method of the invention. This sequence has been chemically
CC synthesised using the codons which are most often used by *E. coli*, to
CC facilitate its expression
XX
SQ Sequence 630 BP; 188 A; 161 C; 143 G; 138 T; 0 U; 0 Other;

Query Match 100.0%; Score 630; DB 6; Length 630;
Best Local Similarity 100.0%; Pred. No. 2.1e-159;
Matches 630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGTAGAGATCGAGATCTCGATCCGCGAAATTAATACGACTCACTATAGGGGAATTGT 60
DB |||||||
QY 1 GCGTAGAGATCGAGATCTCGATCCGCGAAATTAATACGACTCACTATAGGGGAATTGT 60
DB |||||||
QY 61 GAGCGGATAACAATTCCCCTCTAGAAATAATTTGTTAACTTTAAGAGGAGATATACA 120
DB |||||||
QY 61 GAGCGGATAACAATTCCCCTCTAGAAATAATTTGTTAACTTTAAGAGGAGATATACA 120
DB |||||||
QY 121 TATGTTTAACTTCCGCGGGAATTACAAAACCCCAAGCTTCTTACTCGAGTAACGG 180
DB |||||||
QY 121 TATGTTTAACTTCCGCGGGAATTACAAAACCCCAAGCTTCTTACTCGAGTAACGG 180
DB |||||||
QY 181 AGGACACTTCTCGCAATTCGCCAGATGCGACAGTAGATGGGACTCGCGATCGCTCCGA 240
DB |||||||
QY 181 AGGACACTTCTCGCAATTCGCCAGATGCGACAGTAGATGGGACTCGCGATCGCTCCGA 240
DB |||||||
QY 241 CCAGCACATTACGCTGCAACTCTCGGCCGAAAGCGTTGGAGAGGCTTATATCAAGTCGAC 300
DB |||||||
QY 241 CCAGCACATTACGCTGCAACTCTCGGCCGAAAGCGTTGGAGAGGCTTATATCAAGTCGAC 300
DB |||||||
QY 301 GGAGACTGCCAGTACTTGCATGACACCGATGGGCTTCTGTATGGCTACACAGCGC 360
DB |||||||
QY 301 GGAGACTGCCAGTACTTGCATGACACCGATGGGCTTCTGTATGGCTACACAGCGC 360
DB |||||||
QY 361 TAAACGAAGAATGCTTGTCTAGAAAGACTAGAAAGAAACCAATTAACAACCGTACATATC 420
DB |||||||
QY 361 TAAACGAAGAATGCTTGTCTAGAAAGACTAGAAAGAAACCAATTAACAACCGTACATATC 420
DB |||||||
QY 421 GAAAAAATATGAGAGAAAGACTGTTTGTAGGCTTTAAAAAAATTTGTTCTGTAAGCG 480
DB |||||||
QY 421 GAAAAAATATGAGAGAAAGACTGTTTGTAGGCTTTAAAAAAATTTGTTCTGTAAGCG 480
DB |||||||
QY 481 TGGACACGAGTACTATGGCCAAAGGCTATCTTGTTCCTGCGCACTACAGTACGCTC 540
DB |||||||
QY 481 TGGACACGAGTACTATGGCCAAAGGCTATCTTGTTCCTGCGCACTACAGTACGCTC 540
DB |||||||
QY 541 CGACTAAGGATCCGAATTCGAGTCCGTCGACAAAGCTTCCGCGCGGCGGCTCGAGCACC 600
DB |||||||
QY 541 CGACTAAGGATCCGAATTCGAGTCCGTCGACAAAGCTTCCGCGCGGCGGCTCGAGCACC 600
DB |||||||
QY 601 ACCACCACTGAGATCCGGCTGCTTAACA 630
DB |||||||
QY 601 ACCACCACTGAGATCCGGCTGCTTAACA 630
DB |||||||

RESULT 2
AAK98920
ID AAK98920 standard; DNA; 630 BP.
XX

AC AAK98920;
XX
DT 24-MAY-2002. (first entry)
XX
DE Codon optimised DNA of chemically synthesised human A FGF (140AA).
XX
KW Human acidic fibroblast growth factor; phase T7 polymerase promoter;
KW lysis; phase dependent superproduction; A FGF; codon optimisation; gene;
KW ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 122..547
FT /*tag= a
FT /product= "Protein of human A FGF (140AA) "
XX
PN WO200214468-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US025477.
XX
PR 15-AUG-2000; 2000US-0225437P.
XX
PA (PHAG-) PHAGE BIOTECHNOLOGY CORP.
XX
PI Kordyum VA, Chernykh SI, Slavchenko IV, Vozianov OF;
XX
DR WPI; 2002-269184/31.
DR P-PSDB; AAO19992.
XX
PT Bacteriophage-dependent method for producing biologically active proteins
PT or peptides, involves employing an *Escherichia coli* transformed with a
PT plasmid containing the targeted gene(s) operably linked to a promoter.
XX
PS Example 3; Fig 8; 44pp; English.
XX
CC The invention relates to a method for enhancing the production of a
CC biologically active protein comprising infecting a strain of *Escherichia*
CC *coli*, which has been transformed with a plasmid having at least one copy
CC of an expressible gene, such as a human acidic fibroblast growth factor.
CC The expressible gene encodes a biologically active protein operably
CC linked to a phase T7 polymerase promoter, with a bacteriophage capable of
CC mediating delayed lysis. The method is useful for the phage dependent
CC superproduction of biologically active protein and peptides. The method
CC is particularly useful for enhancing the production of heterologous
CC proteins in bacterial host cells. This polynucleotide sequence represents
CC a codon optimised DNA of a chemically synthesised human acidic fibroblast
CC growth factor - human A FGF (140AA) of the invention
XX
SQ Sequence 630 BP; 188 A; 161 C; 143 G; 138 T; 0 U; 0 Other;

Query Match 100.0%; Score 630; DB 6; Length 630;
Best Local Similarity 100.0%; Pred. No. 2.1e-159;
Matches 630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGTAGAGATCGAGATCTCGATCCGCGAAATTAATACGACTCACTATAGGGGAATTGT 60
DB |||||||
QY 1 GCGTAGAGATCGAGATCTCGATCCGCGAAATTAATACGACTCACTATAGGGGAATTGT 60
DB |||||||
QY 61 GAGCGGATAACAATTCCCCTCTAGAAATAATTTGTTTAACTTTAAGAGGAGATATACA 120
DB |||||||
QY 61 GAGCGGATAACAATTCCCCTCTAGAAATAATTTGTTTAACTTTAAGAGGAGATATACA 120
DB |||||||
QY 121 TATGTTTAACTTCCGCGGGAATTACAAAACCCCAAGCTTCTTACTCGAGTAACGG 180
DB |||||||
QY 121 TATGTTTAACTTCCGCGGGAATTACAAAACCCCAAGCTTCTTACTCGAGTAACGG 180
DB |||||||
QY 181 AGGACACTTCTCGCAATTCGCCAGATGCGACAGTAGATGGGACTCGCGATCGCTCCGA 240
DB |||||||
QY 181 AGGACACTTCTCGCAATTCGCCAGATGCGACAGTAGATGGGACTCGCGATCGCTCCGA 240
DB |||||||

QY 241 CCAGCATTTCAGCTGCAACTCTCGSCCGAAGCGTTGGAGAGGTTCTATATCAAGTCGAC 300
DB |||||||
QY 241 CCAGCATTTCAGCTGCAACTCTCGSCCGAAGCGTTGGAGAGGTTCTATATCAAGTCGAC 300
DB |||||||
QY 301 CGAGACTGCGCAGTACTCTTGCCATGACACCGATGGGCTTCTGTATGGCTCACAGACGCC 360
DB |||||||
QY 301 GGAGACTGCGCAGTACTCTTGCCATGACACCGATGGGCTTCTGTATGGCTCACAGACGCC 360
DB |||||||
QY 361 TAACGAAGAAATGCTTGTCTTAGAAGACTAGAGAAACCAATTAACAACGTCATATATC 420
DB |||||||
QY 361 TAACGAAGAAATGCTTGTCTTAGAAGACTAGAGAAACCAATTAACAACGTCATATATC 420
DB |||||||
QY 421 GAAAAAATCGACAGAACTGTTTCTAGGCTTTAAAAAATGGTTCTGTAAAGCG 480
DB |||||||
QY 421 GAAAAAATCGACAGAACTGTTTCTAGGCTTTAAAAAATGGTTCTGTAAAGCG 480
DB |||||||
QY 481 TGGACCAAGCACTCACTATGCGCAAAAGGCTATCTTGTCTGCCACTACCAAGTGAAGTC 540
DB |||||||
QY 481 TGGACCAAGCACTCACTATGCGCAAAAGGCTATCTTGTCTGCCACTACCAAGTGAAGTC 540
DB |||||||
QY 541 CGACTAAGATCGAATTCGAGCTCGTTCGACAAAGCTTGGTCTGCCACTACCAAGTGAAGTC 600
DB |||||||
QY 541 CGACTAAGATCGAATTCGAGCTCGTTCGACAAAGCTTGGTCTGCCACTACCAAGTGAAGTC 600
DB |||||||
QY 601 ACCACCACTGAGATCCGGCTGCTAACA 630
DB |||||||
QY 601 ACCACCACTGAGATCCGGCTGCTAACA 630
DB |||||||

RESULT 3

ID ADO55205 standard; DNA; 630 BP.
XX AC ADO55205;
XX AC ADO55205;
DT 09-SEP-2004 (first entry)
XX DE Human acidic fibroblast growth factor (hAFGF) DNA seqid 4.
XX DE
XX KW neoangiogenesis stimulator; cardiant; vasotropic; revascularisation;
KW ischaemic region; fibroblast growth factor-1; FGF-1; neoangiogenesis;
KW acidic FGF; aFGF; bacteriophage lambda; coronary artery disease;
KW myocardial perfusion; revascularisation therapy; ischaemic myocardium;
KW human; gene; ds.
XX KW
XX OS Homo sapiens.
OS Synthetic.
XX FH
XX Key Location/Qualifiers
CDS 122..547
FT FT /*tag= a
FT FT /product= "hAFGF"
FT FT /note= "human acidic fibroblast growth factor"
XX
XX US2004115769-A1.
XX
XX PD 17-JUN-2004.
XX
XX PF 27-AUG-2003; 2003US-00649480.
XX
XX PR 24-JUL-1998; 98US-0093962P.
PR 22-JUL-1999; 99US-00358780.
PR 15-AUG-2000; 2000US-0225406P.
PR 15-AUG-2001; 2001US-00929945.
XX
XX (STEG/) STEGMANN T J.
FA (KORD/) KORDYUM V A.
FA (SLAV/) SLAVCHENKO I Y.
PA (CHER/) CHERNYKH S I.
PA (VOZI/) VOZIANOV O F.
XX
XX Stegmann TJ, Kordyum VA, Slavchenko IY, Chernykh SI, Vozianov OF;

XX WPI; 2004-449397/42.
DR P-PSDB; ADO55206.
XX
PT Revascularizing an ischemic region, for treating coronary artery disease,
PT comprises preparing and injecting a composition comprising a recombinant
PT human fibroblast growth factor-1 into the ischemic region to induce local
PT neoangiogenesis.
XX
PS Claim 2; SEQ ID NO 6; 42pp; English.
XX
CC The invention describes revascularising an ischaemic region comprising
CC preparing a pharmaceutical composition comprising a recombinant
CC fibroblast growth factor-1 (FGF-1) and injecting an amount of the
CC pharmaceutical composition into the ischaemic region, the amount being
CC sufficient to induce local neoangiogenesis. The FGF-1 is prepared by
CC transforming an Escherichia coli host cell with a plasmid comprising an
CC expressible gene encoding a biologically active human acidic FGF protein,
CC operably linked to a promoter; infecting the transformed bacterial host
CC cell with a bacteriophage λ lgr; which mediates delayed lysis; and
CC culturing the E. coli host cell under a culture condition that induces
CC lytic growth of the cell without lysis until a desired level of
CC production of the protein is reached, where the protein is produced as a
CC soluble, biologically-active human acidic FGF protein. Also described is
CC a method of treating coronary artery disease in a patient, comprising
CC preparing a pharmaceutical composition comprising a recombinant FGF-1;
CC injecting an amount of the pharmaceutical composition into at least one
CC site in a heart wall, the amount being sufficient to improve myocardial
CC perfusion; and injecting a composition comprising a physiological glue to
CC a surface of the heart at the site(s) where the pharmaceutical
CC heart disease by revascularisation therapy or for inducing local
CC neoangiogenesis in ischaemic myocardium. This sequence represents human
CC acidic fibroblast growth factor (hAFGF) DNA which has been modified by
CC substitution of naturally occurring codons with codons found in highly
CC expressed E.coli proteins.
XX
SQ Sequence 630 BP; 188 A; 161 C; 143 G; 138 T; 0 U; 0 Other;

Query Match 100.0%; Score 630; DB 12; Length 630;
Best Local Similarity 100.0%; Pred. No. 2.1e-159;
Matches 630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCTAGAGATCGAGATCTCGATCCCGCGAAATTAATAGCACTCACTATAGGGGAATTGT 60
DB |||||||
QY 1 GCCTAGAGATCGAGATCTCGATCCCGCGAAATTAATAGCACTCACTATAGGGGAATTGT 60
DB |||||||
QY 61 GAGCGGATAAACAATTCCTCTAGAAATAATTTTGTGTTTAACTTAAGAGAGATATACA 120
DB |||||||
QY 121 TATGTTTAACTTCCTCGCGGGAATTAACAATAACCCAGCTTCTTTACTGCAAGTACGG 180
DB |||||||
QY 121 TATGTTTAACTTCCTCGCGGGAATTAACAATAACCCAGCTTCTTTACTGCAAGTACGG 180
DB |||||||
QY 181 AGGACACTTCTCGGAAATTCGCGAGATGCGACAGTAGATGGGACTCGCGATCGCTCCGA 240
DB |||||||
QY 181 AGGACACTTCTCGGAAATTCGCGAGATGCGACAGTAGATGGGACTCGCGATCGCTCCGA 240
DB |||||||
QY 241 CCAGCACATTTCAGCTGCAACTCTCGSCCGAAGCGTTGGAGAGGTTCTATATCAAGTCGAC 300
DB |||||||
QY 241 CCAGCACATTTCAGCTGCAACTCTCGSCCGAAGCGTTGGAGAGGTTCTATATCAAGTCGAC 300
DB |||||||
QY 301 GGAGACTGCGCAGTACTCTTGCCATGACACCGATGGGCTTCTGTATGGCTCACAGACGCC 360
DB |||||||
QY 301 GGAGACTGCGCAGTACTCTTGCCATGACACCGATGGGCTTCTGTATGGCTCACAGACGCC 360
DB |||||||
QY 361 TAACGAAGAAATGCTTGTCTTAGAAGACTAGAGAAACCAATTAACAACGTCATATATC 420
DB |||||||
QY 361 TAACGAAGAAATGCTTGTCTTAGAAGACTAGAGAAACCAATTAACAACGTCATATATC 420
DB |||||||
QY 421 GAAAAAATCGACAGAACTGTTTGTAGGCTTTAAAAAATGGTTCTGTAAAGCG 480
DB |||||||

Db 421 GAAAAAATCATGAGAGAACTGGTTTCTAGGCTTAAAAAATGGTTCTGTAAGCG 480
 QY 481 TGGACCAAGGACTCACTATGCGCAAGGCTATCTGTTCTGCGCACTACGAGTGC 540
 Db 481 TGGACCAAGGACTCACTATGCGCAAGGCTATCTGTTCTGCGCACTACGAGTGC 540
 QY 541 CGACTAAGGATCCGAATTCGAGTCCGTCGACAAAGCTTCGCGCGGCACTCGAGCACC 600
 Db 541 CGACTAAGGATCCGAATTCGAGTCCGTCGACAAAGCTTCGCGCGGCACTCGAGCACC 600
 QY 601 ACCACCACTGAGATCCGGTGTCTAACA 630
 Db 601 ACCACCACTGAGATCCGGTGTCTAACA 630

RESULT 4
 ID ABK10594 standard; cDNA; 630 BP.
 AC ABK10594;
 XX
 DT 05-JUN-2002 (first entry)
 DE cDNA encoding human acidic FGF protein (hAFGF134).
 KW hAFGF134; acidic fibroblast growth factor; cell proliferation;
 KW differentiation; tumorigenesis; metastasis; angiogenesis; chromosome 5;
 KW ss; human.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT CDS 122..529
 FT /*tag= a
 FT /product= "hAFGF 134 protein"
 XX
 WO200214471-A2.
 XX
 XX
 PD 21-FEB-2002.
 PF 15-AUG-2001; 2001WO-US025537.
 PR 15-AUG-2000; 2000US-0225406P.
 XX (PHAG-) PHAGE BIOTECHNOLOGY CORP.
 XX Stegmann TJ, Kordyum VA, Chernykh SI, Slavchenko IV, Vozianov OF;
 PI WPI: 2002-257598/30.
 DR N-PSDB; AAU76944.
 XX

Producing a biologically active human acidic fibroblast growth factor (hAFGF) protein for use in promoting angiogenesis, involves employing an E. coli transformed with a plasmid having an hAFGF gene operably linked to a promoter.
 Example 1; Fig 6; 41pp; English.
 This invention relates to a novel method for producing a biologically active human acidic fibroblast growth factor (hAFGF) protein. Fibroblast growth factors are potent regulators of cell proliferation, differentiation and normal development and they have been shown to play a role in tumorigenesis and metastasis. Acidic fibroblast growth factor has been shown to be potent inducers of angiogenesis. The gene for acidic fibroblast growth factor is located on human chromosome 5. The method of the invention comprises employing a plasmid having at least one copy of the gene, which encodes a biologically active hAFGF protein operably linked to a promoter, to transform Escherichia coli. The method is useful for producing recombinant or biologically active hAFGF protein, which is useful in promoting angiogenesis. The present sequence represents a cDNA encoding the human acidic fibroblast growth factor 134 protein (hAFGF134) used in the method of the invention. This sequence has been chemically

CC synthesised using the codons which are most often used by E. coli, to
 CC facilitate its expression
 XX Sequence 630 BP; 193 A; 158 C; 145 G; 134 T; 0 U; 0 Other;
 SQ Query Match 92.7%; Score 584; DB 6; Length 630;
 Best Local Similarity 97.1%; Pred. No. 5.1e-147;
 Matches 612; Conservative 0; Mismatches 0; Indels 18; Gaps 1;
 QY 1 CGCTAGAGGATCGAGATCTCGATCCGCGGAAATTAATACGACTCACTATAGGGAATTGT 60
 Db 1 CGCTAGAGGATCGAGATCTCGATCCGCGGAAATTAATACGACTCACTATAGGGAATTGT 60
 QY 61 GAGCGGATAACAATTCCTCTAGAAATAATTTTGTAACTTTAAGAGAGATATACA 120
 Db 61 GAGCGGATAACAATTCCTCTAGAAATAATTTTGTAACTTTAAGAGAGATATACA 120
 QY 121 TATGTTTAACTTCGCGCGGGAATTAACAAAAACCCCAAGCTTCTTTACTCAGTAACGG 180
 Db 121 TAT-----GAATTACAAAAACCCCAAGCTTCTTTACTCAGTAACGG 162
 QY 181 AGGACATTTCTGCGAATTTGCGAGATGGCACAGTAGATGGGACTTCGCGATCGCTCCGA 240
 Db 163 AGGACATTTCTGCGAATTTGCGAGATGGCACAGTAGATGGGACTTCGCGATCGCTCCGA 222
 QY 241 CCAGCACATTCAGCTGCAACTCTCGCGCGAAGCGTTGGAGAGGTCTATATCAAGTCGAC 300
 Db 223 CCAGCACATTCAGCTGCAACTCTCGCGCGAAGCGTTGGAGAGGTCTATATCAAGTCGAC 282
 QY 301 GGAGACTGGCCAGTACCTTGCCATGGCACCGATGGGCTTCTGTATGGCTCACAGACGCC 360
 Db 283 GGAGACTGGCCAGTACCTTGCCATGGCACCGATGGGCTTCTGTATGGCTCACAGACGCC 342
 QY 361 TAAAGAAATGCTTGTCTTAGAAAGACTAGAAAGAAACCATTTACAAACAGTCATATC 420
 Db 343 TAAAGAAATGCTTGTCTTAGAAAGACTAGAAAGAAACCATTTACAAACAGTCATATC 402
 QY 421 GAAAAACATCGAGAGAACTGGTTGTAGGCGCTTAAAAAATGGTTCTCTGTAAGCG 480
 Db 403 GAAAAACATCGAGAGAACTGGTTGTAGGCGCTTAAAAAATGGTTCTCTGTAAGCG 462
 QY 481 TGGACCAAGGACTCACTATGCGCAAGGCTATCTTGTCTGCGCACTACCACTGAGCTC 540
 Db 463 TGGACCAAGGACTCACTATGCGCAAGGCTATCTTGTCTGCGCACTACCACTGAGCTC 522
 QY 541 CGACTAAGGATCCGAATTCGAGTCCGTCGACAAAGCTTGGCGCGGCACTCGAGCACCACC 600
 Db 523 CGACTAAGGATCCGAATTCGAGTCCGTCGACAAAGCTTGGCGCGGCACTCGAGCACCACC 582
 QY 601 ACCACCACTGAGATCCGGCTGTAAACA 630
 Db 583 ACCACCACTGAGATCCGGCTGTAAACA 612

RESULT 5
 AAK98919
 ID AAK98919 standard; DNA; 630 BP.
 XX
 AC AAK98919;
 XX
 DT 24-MAY-2002 (first entry)
 DE Codon optimised DNA of chemically synthesised human A FGF (134AA).
 XX Human acidic fibroblast growth factor; phage T7 polymerase promoter;
 KW lysis; phage dependent superproduction; A FGF; codon optimisation; gene;
 KW ds.
 XX Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT CDS 122..529

```

FT      /*tag= a
FX      /product= "Protein of human A FGF (134AA)"
FN
PD      WO200214468-A2.
PP      21-FEB-2002.
PX      15-AUG-2001; 2001WO-US025477.
XX      15-AUG-2000; 2000US-0225437P.
XX      (PHAG-) PHAGE BIOTECHNOLOGY CORP.
PI      Kordyum VA, Chernykh SI, Slavchenko IY, Vozianov OF;
XX      WPI; 2002-269184/31.
DR      P-PSDB; AAO19991.
XX
XX      Bacteriophage-dependent method for producing biologically active proteins
PT      or peptides, involves employing an Escherichia coli transformed with a
PT      plasmid containing the targeted gene(s) operably linked to a promoter.
XX
XX      Example 2; Fig 6; 44pp; English.
XX
XX      The invention relates to a method for enhancing the production of a
CC      biologically active protein comprising infecting a strain of Escherichia
CC      coli, which has been transformed with a plasmid having at least one copy
CC      of an expressible gene, such as a human acidic fibroblast growth factor.
CC      The expressible gene encodes a biologically active protein operably
CC      linked to a phase T7 polymerase promoter, with a bacteriophage capable of
CC      mediating delayed lysis. The method is useful for the phase dependent
CC      superproduction of biologically active protein and peptides. The method
CC      is particularly useful for enhancing the production of heterologous
CC      proteins in bacterial host cells. This polynucleotide sequence represents
CC      a codon optimised DNA of a chemically synthesised human acidic fibroblast
CC      growth factor - human A FGF (134AA) of the invention
XX
XX      Sequence 630 BP; 193 A; 158 C; 145 G; 134 T; 0 U; 0 Other;
SQ
Query Match          92.7%; Score 584; DB 6; Length 630;
Best Local Similarity 97.1%; Pred. No. 5.1e-147;
Matches 612; Conservative 0; Mismatches 0; Indels 18; Gaps 1;

QY      1  GCCTAGAGATCGAGATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGGAATTGT 60
DB      1  GCCTAGAGATCGAGATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGGAATTGT 60
QY      61  GAGCGGTATACAAATTCCTCTAGAAATAATTTTGTAACTTTTAAAGAGGAGATATACA 120
DB      61  GAGCGGTATACAAATTCCTCTAGAAATAATTTTGTAACTTTTAAAGAGGAGATATACA 120
QY      121  TATGTTTAACTTTCCGCGCGGGAATTACAAAAACCCAAAGCTTTCTTTACTGCGATACGG 180
DB      121  TAT-----GAAATTACAAAAACCCAAAGCTTTCTTTACTGCGATACGG 162
QY      181  AGGACATCTCTCGGAATTCGCGAGATGGACAGTAGATGGGACTCGCGATCGCTCCGA 240
DB      163  AGGACATCTCTCGGAATTCGCGAGATGGACAGTAGATGGGACTCGCGATCGCTCCGA 222
QY      241  CCAGCATTCAGTGTCAACTCTCGCGGAAAGGTTGGAGAGTCTATATCAAGTCGAC 300
DB      223  CCAGCATTCAGTGTCAACTCTCGCGGAAAGGTTGGAGAGTCTATATCAAGTCGAC 282
QY      301  GGAGACTGGCCAGTACCTTGCATGGACACCGATGGGCTTCTGTATGGCTCACAGAGCC 360
DB      283  GGAGACTGGCCAGTACCTTGCATGGACACCGATGGGCTTCTGTATGGCTCACAGAGCC 342
QY      361  TAACTGAAGATGCTTTGTTTCTAGAAAGACTAGAGAGAAACCATTTACACGTCATATC 420
DB      343  TAACTGAAGATGCTTTGTTTCTAGAAAGACTAGAGAGAAACCATTTACACGTCATATC 402
QY      421  GAAAAACATGCAGAGAAAGACTGGTTGTAGGCCCTTAAAAAAATGGTTCCTTAGCG 480

```

```

DB      403  GAAAAAACATCGAGAGAGAACTGGTTTGTAGGCTTTAAAAAATGTTCTCTTAAGCG 462
QY      481  TGGACACCGGACTCACTATGGCCAAAGGCTATCTTGTTCCTGCCACTACCACTAGAGTC 540
DB      463  TGGACACCGGACTCACTATGGCCAAAGGCTATCTTGTTCCTGCCACTACCACTAGAGTC 522
QY      541  CGACTAAGGATCCGAATTCGAGCTCCGTCGACAGACTTGGCGCGGCGCACTCGAGCACC 600
DB      523  CGACTAAGGATCCGAATTCGAGCTCCGTCGACAGACTTGGCGCGGCGCACTCGAGCACC 582
QY      601  ACCACCACTCGAGATCCGGCTGCTAACA 630
DB      583  ACCACCACTCGAGATCCGGCTGCTAACA 612

RESULT 6
AD055203
ID      AD055203 standard; DNA; 630 BP.
AC      AD055203;
DX      09-SEP-2004 (first entry)
XX      Human acidic fibroblast growth factor (hAFGF) DNA seqid 4.
DE      neoangiogenesis stimulator; cardiant; vasotropic; revascularisation;
KW      ischaemic region; fibroblast growth factor-1; FGF-1; neoangiogenesis;
KW      acidic FGF; aFGF; bacteriophage lambda; coronary artery disease;
KW      myocardial perfusion; revascularisation therapy; ischaemic myocardium;
KW      human; gene; ds.
XX      Homo sapiens.
OS      Synthetic.
XX
XX      Location/Qualifiers
FH      Key
CDS      122..529
         /*tag= a
         /product= "hAFGF"
         /note= "human acidic fibroblast growth factor"
US2004115769-A1.
17-JUN-2004.
27-AUG-2003; 2003US-00649480.
24-JUL-1998; 98US-0093962P.
22-JUL-1999; 99US-00358780.
15-AUG-2000; 2000US-0225406P.
15-AUG-2001; 2001US-00929945.
(STEG/) STEGMANN T J.
(KORD/) KORDYUM V A.
(SLAV/) SLAVCHENKO I Y.
(ChER/) CHERNYKH S I.
(VOZI/) VOZIANOV O F.
Stegmann TJ, Kordyum VA, Slavchenko IY, Chernykh SI, Vozianov OF;
WPI; 2004-449397/42.
Revascularizing an ischemic region, for treating coronary artery disease,
comprises preparing and injecting a composition comprising a recombinant
human fibroblast growth factor-1 into the ischemic region to induce local
neoangiogenesis.
Claim 2; SEQ ID NO 4; 42pp; English.
The invention describes revascularising an ischaemic region comprising
preparing a pharmaceutical composition comprising a recombinant
fibroblast growth factor-1 (FGF-1) and injecting an amount of the
pharmaceutical composition into the ischaemic region, the amount being
sufficient to induce local neoangiogenesis. The FGF-1 is prepared by

```

transforming an *Escherichia coli* host cell with a plasmid comprising an expressible gene encoding a biologically active human acidic FGF protein, CC operably linked to a promoter; infecting the transformed bacterial host CC cell with a bacteriophage ϕ lgr; which mediates delayed lysis; and CC cultivating the *E. coli* host cell under a culture condition that induces CC lytic growth of the cell without lysis until a desired level of CC production of the protein is reached, where the protein is produced as a CC soluble, biologically-active human acidic FGF protein. Also described is CC a method of treating coronary artery disease in a patient, comprising CC preparing a pharmaceutical composition comprising a recombinant FGF-1; CC injecting an amount of the pharmaceutical composition into at least one CC site in a heart wall, the amount being sufficient to improve myocardial CC perfusion; and injecting a composition comprising a physiological glue to CC a surface of the heart at the site(s) where the pharmaceutical CC composition was injected. The methods are useful for treating coronary CC heart disease by revascularisation therapy or for inducing local CC neoangiogenesis in ischaemic myocardium. This sequence represents human CC acidic fibroblast growth factor (hAFGF) DNA which has been modified by CC substitution of naturally occurring codons with codons found in highly CC expressed *E. coli* proteins.

SQ Sequence 630 BP; 193 A; 158 C; 145 G; 134 T; 0 U; 0 Other;
Query Match 92.7%; Score 584; DB 12; Length 630;
Best Local Similarity 97.1%; Pred. No. 5.1e-14;
Matches 612; Conservative 0; Mismatches 0; Indels 18; Gaps 1

Qy	1	CGGTAGAGATCGAGATCTCGATCCGGGAAATTAATACGATCACTATAGGGGAATTGT	60
Db	1	CGGTAGAGATCGAGATCTCGATCCGGGAAATTAATACGATCACTATAGGGGAATTGT	60
Qy	61	GAGCGGATAACAAATTCCTCTPAGAAATAATTTGTTTAACTTTAAGAGGAGATATACA	120
Db	61	GAGCGGATACAAATTCCTCTPAGAAATAATTTGTTTAACTTTAAGAGGAGATATACA	120
Qy	121	TATGTTTAACTTCCGCCCGGGAAATTACAAAACCCCAAGCTTCTTTACTGCAGTAAACGG	180
Db	121	TAT-----GAAATTACAAAACCCCAAGCTTCTTTACTGCAGTAAACGG	162
Qy	181	AGGACACTTCCTGCGAATTCGCCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCGA	240
Db	163	AGGACACTTCCTGCGAATTCGCCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCGA	222
Qy	241	CCAGCACATTCAGCTGCAACTCTCGCGCGAAAGCGTTGGAGAGGCTATATCAAGTCGAC	300
Db	223	CCAGCACATTCAGCTGCAACTCTCGCGCGAAAGCGTTGGAGAGGCTATATCAAGTCGAC	282
Qy	301	GGAGACTGGCAGTACCTTGGCCATCGACACCGATGGGCTTCTGTATGGTCTACAGACGCC	360
Db	283	GGAGACTGGCCAGTACCTTGGCCATCGACACCGATGGGCTTCTGTATGGTCTACAGACGCC	342
Qy	361	TAA CGAAGAATCTTGTTTCTAGAAAGACTAGAAGAAAACCAATTACAACACCTACATATC	420
Db	343	TAA CGAAGATCTGTTTCTTAGAAGACTAGAAGAAAACCAATTACAACACCTACATATC	402
Qy	421	GAATAAACATGCAGAGAAGAACTGGTGTGTAGGCCCTTAAAAAAATGGTTCCTGTAAAGCG	480
Db	403	GAATAAACATGCAGAGAAGAACTGGTGTGTAGGCCCTTAAAAAAATGGTTCCTGTAAAGCG	462
Qy	481	TGGACCA CGGACTCACTATGGCCAAAGGCTATCTGTTCCTGCCACTACCACTGAGCTC	540
Db	463	TGGACCA CGGACTCACTATGGCCAAAGGCTATCTGTTCCTGCCACTACCACTGAGCTC	522
Qy	541	CGACTAAGGATCCGAATTCGAGCTCCGTCGACAAAGCTTGGCGGCGGCACCTCGAGCACCCAC	600
Db	523	CGACTAAGGATCCGAATTCGAGCTCCGTCGACAAAGCTTGGCGGCGGCACCTCGAGCACCCAC	582
Qy	601	ACCACCA CCACTGAGATCCGGTGTCTAAC	630
Db	583	ACCACCA CCACTGAGATCCGGTGTCTAAC	612

RESULT 7

AAK98922	AAK98922 standard; DNA; 990 BP.
XX AC	AAK98922;
XX DT	24-MAY-2002 (first entry)
XX DE	Codon optimised synthetic gene encoding human interferon alpha-2b.
XX KW	Human acidic fibroblast growth factor; phage T7 polymerase promoter;
XX KW	lysis; phage dependent superproduction; synthetic; growth hormone; gene;
XX KW	human interferon alpha-2b; codon optimisation; ds.
XX OS	Homo sapiens.
XX OS	Synthetic.
XX FH	Key Location/Qualifiers
XX FT	promoter 231..249
XX FT	misc_signal /*tag= b
XX FT	250..274
XX FT	/*tag= c
XX FT	/note= "Operator sequence"
XX FT	320..787
XX FT	/*tag= a
XX FT	/product= "Protein of a human interferon alpha-2b"
XX PN	WO200214468-A2.
XX PD	21-FEB-2002.
XX XX	15-AUG-2001; 2001WO-US025477.
XX PF	15-AUG-2000; 2000US-0225437P.
XX PR	(PHAG-) PHAGE BIOTECHNOLOGY CORP.
XX PA	Kordyum VA, Chernykh SI, Slavchenko IY, Vozianov OF;
XX FI	WPI; 2002-269184/31.
XX DR	P-PSDB; RAO19994.
XX DR	Bacteriophage-dependent method for producing biologically active proteins
XX PT	or peptides, involves employing an Escherichia coli transformed with a
XX PT	plasmid containing the targeted gene(s) operably linked to a promoter.
XX PS	Example 8; Fig 10; 44pp; English.
XX CC	The invention relates to a method for enhancing the production of a
XX CC	biologically active protein comprising infecting a strain of Escherichia
XX CC	coli, which has been transformed with a plasmid having at least one copy
XX CC	of an expressible gene, such as a human acidic fibroblast growth factor.
XX CC	The expressible gene encodes a biologically active protein operably
XX CC	linked to a phage T7 polymerase promoter, with a bacteriophage capable of
XX CC	mediating delayed lysis. The method is useful for the phage dependent
XX CC	superproduction of biologically active protein and peptides. The method
XX CC	is particularly useful for enhancing the production of heterologous
XX CC	proteins in bacterial host cells. This polynucleotide sequence represents
XX CC	a codon optimised synthetic gene encoding human interferon alpha-2b of
XX CC	the invention
XX SQ	Sequence 990 BP; 275 A; 262 C; 239 G; 214 T; 0 U; 0 Other;
XX	Query Match 90.1%; Score 567.4; DB 6; Length 990;
XX	Best Local Similarity 92.8%; Pred. No. 1.7e-142;
XX	Matches 623; Conservative 0; Mismatches 6; Indels 42; Gaps 1
QY	2 CGTAGAGGATCGAGATCTCGATCCGCGAAATTAATACGACTCACTATAGGGAATTGTG 61
DB	200 CGTGGCGCGCAGATCTCGATCCGCGAAATTAATACGACTCACTATAGGGAATTGTG 259
QY	62 AGCGGATAACAATTTCCCTCTAGAAAATAATTTTGTTAACTTTAAGAGGAGATATACAT 121
DB	260 AGCGGATAACAATTTCCCTCTAGAAAATAATTTTGTTAACTTTAAGAGGAGATATACAT 319

```
QY 122 ATG-----TTTAACTTCGCCC 139
DB 320 ATGGCTGAAGGGGAATCATCCACCTTTACAGCGTTAAACCGAGAAATTTAACTTCGCCC 379
QY 140 GGGATTACAAAAACCCAAAGCTTCTTACTGAGTAACGGAGGACACTTCCTCGCAATT 199
DB 380 GGGATTACAAAAACCCAAAGCTTCTTACTGAGTAACGGAGGACACTTCCTCGCAATT 439
QY 200 CTGCCAGATGGCACAGTAGATGGGACTCGCGATCGCTCGACGACATTCAGCTGCAA 259
DB 440 CTGCCAGATGGCACAGTAGATGGGACTCGCGATCGCTCGACGACATTCAGCTGCAA 499
QY 260 CTCTCGCGCAAGCGTTGGAGAGGCTTATATCAAGTCGACGAGACTGCGCAGTACCTT 319
DB 500 CTCTCGCGCAAGCGTTGGAGAGGCTTATATCAAGTCGACGAGACTGCGCAGTACCTT 559
QY 320 GCCATGGACACCGATGGCTTCTGTATGGCTCACAGACGCTTAACGAAAGATGCTTTGTT 379
DB 560 GCCATGGACACCGATGGCTTCTGTATGGCTCACAGACGCTTAACGAAAGATGCTTTGTT 619
QY 380 CTAGAAGACTAGAGAAACCAATTACACACGTATATCGAAAAACATGACAGAGAG 439
DB 620 CTAGAAGACTAGAGAAACCAATTACACACGTATATCGAAAAACATGACAGAGAG 679
QY 440 AACTGGTTTGTAGGCTTAAAAAATGTTCTGTAAAGCGTGGACCGGACTCACTAT 499
DB 680 AACTGGTTTGTAGGCTTAAAAAATGTTCTGTAAAGCGTGGACCGGACTCACTAT 739
QY 500 GGCCAAAGGCTATCTTGTCTCGCACACTACGAGTCCGACTAAGGATCCGAATTC 559
DB 740 GGCCAAAGGCTATCTTGTCTCGCACACTACGAGTCCGACTAAGGATCCGAATTC 799
QY 560 GAGTCCGTCGACAAAGCTTGGCGCGCACTCGAGCACACCAACCAACCACTGAGATCC 619
DB 800 GAGTCCGTCGACAAAGCTTGGCGCGCACTCGAGCACACCAACCAACCACTGAGATCC 859
QY 620 GGCTGTAAACA 630
DB 860 GGCTGTAAACA 870

RESULT 8
ID ABK10592 standard; cDNA; 630 BP.
AC ABK10592;
DE 05-JUN-2002 (first entry)
XX cDNA encoding human acidic FGF protein HAFGF155.
XX HAFGF155; acidic fibroblast growth factor; cell proliferation;
XX differentiation; tumorigenesis; metastasis; angiogenesis; chromosome 5;
XX ss; human.
XX Homo sapiens.
XX Synthetic.
XX Key Location/Qualifiers
XX CDS 122..589
XX FT /*tag= a
XX FT /product= "HafGF 155 protein"
XX WO200214471-A2.
XX PD 21-FEB-2002.
XX 15-AUG-2001; 2001WO-US025537.
XX 15-AUG-2000; 2000US-0225406P.
XX (PHAG-) PHAGE BIOTECHNOLOGY CORP.
PA
```

```
XX Stegmann TJ, Kordyum VA, Chernykh SI, Slavchenko IY, Vozianov OF;
PI WPI: 2002-257598/30.
XX P-PSDB; AAU6943.
XX Producing a biologically active human acidic fibroblast growth factor
PT (hafGF) protein for use in promoting angiogenesis, involves employing an
PT E. coli transformed with a plasmid having an hafGF gene operably linked
PT to a promoter.
XX Example 1; Fig 1; 41pp; English.
XX This invention relates to a novel method for producing a biologically
CC active human acidic fibroblast growth factor (hafGF) protein. Fibroblast
CC growth factors are potent regulators of cell proliferation,
CC differentiation and normal development and they have been shown to play a
CC role in tumorigenesis and metastasis. Acidic fibroblast growth factor
CC has been shown to be potent inducers of angiogenesis. The gene for acidic
CC fibroblast growth factor is located on human chromosome 5. The method of
CC the invention comprises employing a plasmid having at least one copy of
CC gene, which encodes a biologically active hafGF protein operably linked
CC to a promoter, to transform Escherichia coli. The method is useful for
CC producing recombinant or biologically active hafGF protein, which is
CC useful in promoting angiogenesis. The present sequence represents a cDNA
CC encoding the human acidic fibroblast growth factor 155 protein (hafGF155)
CC used in the method of the invention. This sequence has been chemically
CC synthesised using the codons which are most often used by E. coli, to
CC facilitate its expression
XX Sequence 630 BP; 191 A; 152 C; 147 G; 140 T; 0 U; 0 Other;
SQ Query Match 85.1%; Score 536; DB 6; Length 630;
Best Local Similarity 93.3%; Pred. No. 4.3e-134;
Matches 588; Conservative 0; Mismatches 0; Indels 42; Gaps 1;
QY 1 GCCTAGAGGATCGAGATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGGAATTGT 60
DB 1 GCCTAGAGGATCGAGATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGGAATTGT 60
QY 61 GAGCGGATTAACAAATTCCTCTAGAAATTAATTTGTTTAACTTAAGAGGAGATATACA 120
DB 61 GAGCGGATTAACAAATTCCTCTAGAAATTAATTTGTTTAACTTAAGAGGAGATATACA 120
QY 121 TATG-----TTTAACTTCGCCC 138
DB 121 TATGGCTGAAGGGGAATCACCACCTTTACAGGTTAACGGAGAAATTTAACTTCGCCC 180
QY 139 CGGGAATTACAAAAACCCAAAGCTTCTTTACTCAGTAACGGAGGACACTTCCTCGCAAT 198
DB 181 CGGGAATTACAAAAACCCAAAGCTTCTTTACTCAGTAACGGAGGACACTTCCTCGCAAT 240
QY 199 TCTGCCAGATGGCACAGTAGATGGGACTCGGATCGCTCGACGACGACATTCAGCTGCA 258
DB 241 TCTGCCAGATGGCACAGTAGATGGGACTCGGATCGCTCGACGACGACATTCAGCTGCA 300
QY 259 ACTCTCGCCGAAAGCGTTGGAGAGGCTATATCAAGTCACGAGAGCTGCCAGTAGTACCT 318
DB 301 ACTCTCGCCGAAAGCGTTGGAGAGGCTATATCAAGTCACGAGAGCTGCCAGTAGTACCT 360
QY 319 TGGCATGGACACCGATGGGCTTCTGTATGGCTCACAGACGCTTAACGAAAGATCTTGT 378
DB 361 TGGCATGGACACCGATGGGCTTCTGTATGGCTCACAGACGCTTAACGAAAGATCTTGT 420
QY 379 TCTAGAAAAGACTAGAGAAACCAATTACACACGTACATATCGAAAAACATGACAGAA 438
DB 421 TCTAGAAAAGACTAGAGAAACCAATTACACACGTACATATCGAAAAACATGACAGAA 480
QY 439 GAACTGGTTTGTAGGCTTAAAAAATGTTCTCTGTAAGCGTGACACCGAGTCACTA 498
DB 481 GAACTGGTTTGTAGGCTTAAAAAATGTTCTCTGTAAGCGTGACACCGAGTCACTA 540
QY 499 TGGCCAAAAGGCTATCTTGTCTTCCTGCCACTACCACTGAGCTCCGACTAAGGATCCGAATT 558
```

Db 541 TGGCCAAAAGGCTATCTTTGCTGCGCACTACGATCGAGCTCGGTAAGGATCCGAAATT 600

QY 559 CGAGCTCCGTCGACAAAGCTTGGCGCGCGAC 588

Db 601 CGAGCTCCGTCGACAAAGCTTGGCGCGCGAC 630

RESULT 9

AAK98917

ID AAK98917 standard; DNA; 630 BP.

AC AAK98917;

XX 24-MAY-2002 (first entry)

DE Codon optimised synthetic human acidic fibroblast growth factor (155AA).

DE Human acidic fibroblast growth factor; phage T7 polymerase promoter;

KW lysis; phage dependent superproduction; synthetic; codon optimisation;

KW gene; ds.

XX Homo sapiens.

OS Synthetic.

PH Key Location/Qualifiers

FT 122..589

FT /tag= a

FT /product= "Protein of human acidic fibroblast growth

FT factor (155AA)"

XX WO200214468-A2.

XX 21-FEB-2002.

XX 15-AUG-2001; 2001WO-US025477.

XX 15-AUG-2000; 2000US-0225437P.

XX (PHAG-) PHAGE BIOTECHNOLOGY CORP.

XX Kordyum VA, Chernykh SI, Slavchenko IY, Vozianov OF;

XX WPI; 2002-269184/31.

DR F-PSDB; AAOL9990.

XX Bacteriophage-dependent method for producing biologically active proteins

PT or peptides, involves employing an Escherichia coli transformed with a

PT plasmid containing the targeted gene(s) operably linked to a promoter.

XX Claim 23; Fig 1; 44pp; English.

XX The invention relates to a method for enhancing the production of a

CC biologically active protein comprising infecting a strain of Escherichia

CC coli, which has been transformed with a plasmid having at least one copy

CC of an expressible gene, such as a human acidic fibroblast growth factor.

CC The expressible gene encodes a biologically active protein operably

CC linked to a phage T7 polymerase promoter, with a bacteriophage capable of

CC mediating delayed lysis. The method is useful for the phage dependent

CC superproduction of biologically active protein and peptides. The method

CC is particularly useful for enhancing the production of heterologous

CC proteins in bacterial host cells. This polynucleotide sequence represents

CC codon optimised DNA of a synthetic human acidic growth factor (155AA) of

CC the invention. This sequence is an alternative coding sequence for SEQ ID

CC 2 (AAO19990)

XX Sequence 630 BP; 191 A; 152 C; 147 G; 140 T; 0 U; 0 Other;

SQ

Query Match 85.1%; Score 536; DB 6; Length 630;

Best Local Similarity 93.3%; Pred. No. 4.3e-134;

Matches 588; Conservative 0; Mismatches 0; Indels 42; Gaps 1;

QY 1 GCGTAGAGGATCGAGATCTCGATCCCGGAAATTAATACGACTCATTAGGGGAATTGT 60

Db 1 GCGTAGAGGATCGAGATCTCGATCCCGGAAATTAATACGACTCATTAGGGGAATTGT 60

QY 61 GAGCGGATAACAATTTCCCTCTAGAAAATAATTTTGTAACTTTAAGAGGAGATATACA 120

Db 61 GAGCGGATAACAATTTCCCTCTAGAAAATAATTTTGTAACTTTAAGAGGAGATATACA 120

QY 121 TATG-----TTTAACTTCCGCC 138

Db 121 TATGGCTGAAGGGGAAATCACCACTTTACAGCGTTAACGGAGAAATTTAACTTCCGCC 180

QY 139 CGGGAATTTACAAAACCCCAAGCTTCTTTACTGCAGTAACCGAGGACACTTCTCCGCAAT 198

Db 181 CGGGAATTTACAAAACCCCAAGCTTCTTTACTGCAGTAACCGAGGACACTTCTCCGCAAT 240

QY 199 TCTGCAGATGGCAGTAGATGGGACTCGCGATCGCTCCGACGAGCAATTCAGCTGCA 258

Db 241 TCTGCCAGATGGCAGTAGATGGGACTCGCGATCGCTCCGACGAGCAATTCAGCTGCA 300

QY 259 ACTCTCGGCCGAAAGCGTTGGAGAGTCTATATCAAGTCGACGGAGACTGGCCAGTACCT 318

Db 301 ACTCTCGGCCGAAAGCGTTGGAGAGTCTATATCAAGTCGACGGAGACTGGCCAGTACCT 360

QY 319 TGCCATGGACACCGATGGGCTTCTGTATGGCTCACAGACGCTAACGAAGAATGCTTGT 378

Db 361 TGCCATGGACACCGATGGGCTTCTGTATGGCTCACAGACGCTAACGAAGAATGCTTGT 420

QY 379 TCTAGAAAGACTAGAGAAAACCATTTACACACATACATATCGAAAAACATGCAGAGAA 438

Db 421 TCTAGAAAGACTAGAGAAAACCATTTACACACATACATATCGAAAAACATGCAGAGAA 480

QY 439 GAACCTGGTTTGTAGGCTTAAAAAATGGTTCTGTAAAGCGTGGACACCGACTCATA 498

Db 481 GAACCTGGTTTGTAGGCTTAAAAAATGGTTCTGTAAAGCGTGGACACCGACTCATA 540

QY 499 TGGCCAAAAGGCTATCTTTGTTCTTGGCCACTACCGAGTCCGACTAAGGATCCGAATT 558

Db 541 TGGCCAAAAGGCTATCTTTGTTCTTGGCCACTACCGAGTCCGACTAAGGATCCGAATT 600

QY 559 CGAGCTCCGTCGACAAAGCTTGGCGCGCGAC 588

Db 601 CGAGCTCCGTCGACAAAGCTTGGCGCGCGAC 630

RESULT 10

ADO55200

ID ADO55200 standard; DNA; 630 BP.

XX AC ADO55200;

XX 09-SEP-2004 (first entry)

XX Human acidic fibroblast growth factor (haFGF) DNA seqid 1.

DE neangiogenesis stimulator; cardiant; vasotropic; revascularisation;

KW ischaemic region; fibroblast growth factor-1; FGF-1; neangiogenesis;

KW acidic FGF; arGF; bacteriophage lambda; coronary artery disease;

KW myocardial perfusion; revascularisation therapy; ischaemic myocardium;

XX human; gene; ds.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT 122..589

FT /tag= a

FT /product= "haFGF"

FT /note= "human acidic fibroblast growth factor"

FT 125..589

FT /tag= b

FT /product= "processed haFGF"

FT /note= "human acidic fibroblast growth factor"

FT /partial

```

121 TATGCTGAAGGGGAAATCACACCTTTACAGCGTTTAAACGGAGAAATTTAACTTCCGCC 180
139 CGGGAATTTACAAAAACCAAGCTTCTTTACTGCACTAAACGGAGGACACTTCTCTCGGAAT 198
181 CGGGAATTTACAAAAACCAAGCTTCTTTACTGCACTAAACGGAGGACACTTCTCTCGGAAT 240
199 TCTGCCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCGACACAGCATTTCAGCTGCA 258
241 TCTGCCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCGACACAGCATTTCAGCTGCA 300
259 ACTCTCGGCGGAAACCGCTTGTAGAGGCTTATATCAAGTCGAGGAGACTTGGCCAGTACCT 318
301 ACTCTCGGCGGAAACCGCTTGTAGAGGCTTATATCAAGTCGAGGAGACTTGGCCAGTACCT 360
319 TGCCATGGACACCGATGGCTTCTGTATGGCTTCACAGACGCTTAAACGAAGAAATGCTTGT 378
361 TGCCATGGACACCGATGGCTTCTGTATGGCTTCACAGACGCTTAAACGAAGAAATGCTTGT 420
379 TCTAGAAAGACTAGAGAAACCATTTACAACAGCTACATATCGAAAAAACAATGCGAGAA 438
421 TCTAGAAAGACTAGAGAAACCATTTACAACAGCTACATATCGAAAAAACAATGCGAGAA 480
439 GAACCTGGTTTGTAGGCTTTAAAAAATGGTTCTTGTAAAGCGTGGACCGGACTCACTA 498
481 GAACCTGGTTTGTAGGCTTTAAAAAATGGTTCTTGTAAAGCGTGGACCGGACTCACTA 540
499 TGGCCAAAAGGCTATCTTCTCTCCACTACAGTAGCTCCGACTAAGGATCCGAAAT 558
541 TGGCCAAAAGGCTATCTTCTCTCCACTACAGTAGCTCCGACTAAGGATCCGAAAT 600
559 CGAGCTCCCTCGACAAAGCTTGGCGCGCAC 588
601 CGAGCTCCCTCGACAAAGCTTGGCGCGCAC 630

RESULT 11
AAT12907
ID AAT12907 standard; cDNA; 8501 BP.
AC AAT12907;
XX
DT 05-NOV-1996 (first entry)
XX
DE Novel expression plasmid pXL2435.
XX
KW Expression vector; T7 phage; gene 10; promoter; heterologous; circular;
transcriptional terminator; plasmid stability region; RP4; maintenance;
plasmid loss; antibiotic resistance; selection; pharmaceutical;
agricultural; biocatalysis; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 6038..8499
FT /tag= a
FT /note= "contains sequence derived from par region of
FT plasmid RP4"
XX
XX WO9608572-A1.
XX
XX 21-MAR-1996.
XX
XX 14-SEP-1995; 95WO-FR001178.
XX
XX 16-SEP-1994; 94FR-00011049.
XX
XX (RHON ) RHONE POULENC RORER SA.
XX
XX Cameron B, Crouzet J;
XX
XX WPI; 1996-179946/18.
XX
XX Expression 'plasmids contg. phage T7 promoter - and stabilising par region

```

```

121 TATGCTGAAGGGGAAATCACACCTTTACAGCGTTTAAACGGAGAAATTTAACTTCCGCC 180
139 CGGGAATTTACAAAAACCAAGCTTCTTTACTGCACTAAACGGAGGACACTTCTCTCGGAAT 198
181 CGGGAATTTACAAAAACCAAGCTTCTTTACTGCACTAAACGGAGGACACTTCTCTCGGAAT 240
199 TCTGCCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCGACACAGCATTTCAGCTGCA 258
241 TCTGCCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCGACACAGCATTTCAGCTGCA 300
259 ACTCTCGGCGGAAACCGCTTGTAGAGGCTTATATCAAGTCGAGGAGACTTGGCCAGTACCT 318
301 ACTCTCGGCGGAAACCGCTTGTAGAGGCTTATATCAAGTCGAGGAGACTTGGCCAGTACCT 360
319 TGCCATGGACACCGATGGCTTCTGTATGGCTTCACAGACGCTTAAACGAAGAAATGCTTGT 378
361 TGCCATGGACACCGATGGCTTCTGTATGGCTTCACAGACGCTTAAACGAAGAAATGCTTGT 420
379 TCTAGAAAGACTAGAGAAACCATTTACAACAGCTACATATCGAAAAAACAATGCGAGAA 438
421 TCTAGAAAGACTAGAGAAACCATTTACAACAGCTACATATCGAAAAAACAATGCGAGAA 480
439 GAACCTGGTTTGTAGGCTTTAAAAAATGGTTCTTGTAAAGCGTGGACCGGACTCACTA 498
481 GAACCTGGTTTGTAGGCTTTAAAAAATGGTTCTTGTAAAGCGTGGACCGGACTCACTA 540
499 TGGCCAAAAGGCTATCTTCTCTCCACTACAGTAGCTCCGACTAAGGATCCGAAAT 558
541 TGGCCAAAAGGCTATCTTCTCTCCACTACAGTAGCTCCGACTAAGGATCCGAAAT 600
559 CGAGCTCCCTCGACAAAGCTTGGCGCGCAC 588
601 CGAGCTCCCTCGACAAAGCTTGGCGCGCAC 630

RESULT 11
AAT12907
ID AAT12907 standard; cDNA; 8501 BP.
AC AAT12907;
XX
DT 05-NOV-1996 (first entry)
XX
DE Novel expression plasmid pXL2435.
XX
KW Expression vector; T7 phage; gene 10; promoter; heterologous; circular;
transcriptional terminator; plasmid stability region; RP4; maintenance;
plasmid loss; antibiotic resistance; selection; pharmaceutical;
agricultural; biocatalysis; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 6038..8499
FT /tag= a
FT /note= "contains sequence derived from par region of
FT plasmid RP4"
XX
XX WO9608572-A1.
XX
XX 21-MAR-1996.
XX
XX 14-SEP-1995; 95WO-FR001178.
XX
XX 16-SEP-1994; 94FR-00011049.
XX
XX (RHON ) RHONE POULENC RORER SA.
XX
XX Cameron B, Crouzet J;
XX
XX WPI; 1996-179946/18.
XX
XX Expression 'plasmids contg. phage T7 promoter - and stabilising par region

```

```

121 TATGCTGAAGGGGAAATCACACCTTTACAGCGTTTAAACGGAGAAATTTAACTTCCGCC 180
139 CGGGAATTTACAAAAACCAAGCTTCTTTACTGCACTAAACGGAGGACACTTCTCTCGGAAT 198
181 CGGGAATTTACAAAAACCAAGCTTCTTTACTGCACTAAACGGAGGACACTTCTCTCGGAAT 240
199 TCTGCCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCGACACAGCATTTCAGCTGCA 258
241 TCTGCCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCGACACAGCATTTCAGCTGCA 300
259 ACTCTCGGCGGAAACCGCTTGTAGAGGCTTATATCAAGTCGAGGAGACTTGGCCAGTACCT 318
301 ACTCTCGGCGGAAACCGCTTGTAGAGGCTTATATCAAGTCGAGGAGACTTGGCCAGTACCT 360
319 TGCCATGGACACCGATGGCTTCTGTATGGCTTCACAGACGCTTAAACGAAGAAATGCTTGT 378
361 TGCCATGGACACCGATGGCTTCTGTATGGCTTCACAGACGCTTAAACGAAGAAATGCTTGT 420
379 TCTAGAAAGACTAGAGAAACCATTTACAACAGCTACATATCGAAAAAACAATGCGAGAA 438
421 TCTAGAAAGACTAGAGAAACCATTTACAACAGCTACATATCGAAAAAACAATGCGAGAA 480
439 GAACCTGGTTTGTAGGCTTTAAAAAATGGTTCTTGTAAAGCGTGGACCGGACTCACTA 498
481 GAACCTGGTTTGTAGGCTTTAAAAAATGGTTCTTGTAAAGCGTGGACCGGACTCACTA 540
499 TGGCCAAAAGGCTATCTTCTCTCCACTACAGTAGCTCCGACTAAGGATCCGAAAT 558
541 TGGCCAAAAGGCTATCTTCTCTCCACTACAGTAGCTCCGACTAAGGATCCGAAAT 600
559 CGAGCTCCCTCGACAAAGCTTGGCGCGCAC 588
601 CGAGCTCCCTCGACAAAGCTTGGCGCGCAC 630

RESULT 11
AAT12907
ID AAT12907 standard; cDNA; 8501 BP.
AC AAT12907;
XX
DT 05-NOV-1996 (first entry)
XX
DE Novel expression plasmid pXL2435.
XX
KW Expression vector; T7 phage; gene 10; promoter; heterologous; circular;
transcriptional terminator; plasmid stability region; RP4; maintenance;
plasmid loss; antibiotic resistance; selection; pharmaceutical;
agricultural; biocatalysis; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 6038..8499
FT /tag= a
FT /note= "contains sequence derived from par region of
FT plasmid RP4"
XX
XX WO9608572-A1.
XX
XX 21-MAR-1996.
XX
XX 14-SEP-1995; 95WO-FR001178.
XX
XX 16-SEP-1994; 94FR-00011049.
XX
XX (RHON ) RHONE POULENC RORER SA.
XX
XX Cameron B, Crouzet J;
XX
XX WPI; 1996-179946/18.
XX
XX Expression 'plasmids contg. phage T7 promoter - and stabilising par region

```



```

RESULT 13
AAQ03873
ID AAQ03873 standard; cDNA; 454 BP.
XX
XX AAQ03873;
AC
XX
XX
DT 22-AUG-1990 (first entry)
XX
XX
DE Synthetic gene encoding human acidic fibroblast growth factor (aFGF).
DE
DE Acidic fibroblast growth factor; aFGF; thrombogenesis; atherosclerosis;
KW tumors; ds.
KW
XX
XX Homo sapiens.
OS
XX GB2223496-A.
PN
XX 11-APR-1990.
PD
XX
XX 08-AUG-1988; 88GB-00018775.
XX
XX 08-AUG-1988; 88GB-00018775.
XX
XX (BRBI-) BRIT BIO-TECH LTD.
PA
XX
XX Davies JA, Johnson ID;
PI
XX WPI; 1990-109882/15.
DR
XX P-PSDB; AAR05789.
DR
XX
XX Gene encoding human acidic fibroblast growth factor - incorporates useful
PT restriction sites at frequent intervals to facilitate cassette
PT mutagenesis of specified regions.
XX
XX Claim 2; Fig 3a; 12pp; English.
XX
XX Gene contains several sets of restriction sites, allowing for cassette
CC mutagenesis. The product prevents thrombogenesis in blood vessels and is
CC important in atherosclerosis and tumor growth
CC
XX
XX Sequence 454 BP; 127 A; 110 C; 119 G; 98 T; 0 U; 0 Other;
SQ
Query Match 46.0%; Score 290; DB 2; Length 454;
Best Local Similarity 80.0%; Pred. No. 6.7e-68;
Matches 341; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

122 ATGTTTAACTTCGCGCGGAATTACAAAACCCCAAGCTTCTTTACTGAGTAACGGA 181
14 ATGTTTAACTTCGCGCGGAATTACAAAACCCCAAGCTTCTTTACTGAGTAACGGA 73
182 GGACACTTCTCGCAATTCGCCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCGAC 241
74 GGCCACTTCTGAGGATTCCTCCGATGGCACAGTAGATGGGACTCGCGATCGCTCCGAC 133
242 CAGCACATTCAGTGCACACTCTCGCGCGAAGAGCTTGAGAGGCTTATATCAAGTCCGAC 301
134 CAGCACATTCAGTGCACACTCTCGCGCGAAGAGCTTGAGAGGCTTATATCAAGTCCGAC 193
302 GAGACTGGCAGTACCTTGCCATGGACACCGATGGCTTCTGTATGGCTCACAGACGCT 361
194 GAGACTGGCAGTACCTTGCCATGGACACCGATGGCTTCTGTATGGCTCACAGACGCT 253
362 AACGAAGATCTGTTTCTAGAAGACTAGAAACCAACATTACAAACGCTACATATCG 421
254 AATGAGGATGTTTCTGGAAGGCTGAGGAGACCAATTACACACTATATATCC 313
422 AAAAACAATGCAGAGAAGACTGGTTTGTAGCCCTTAAAAAATATGGTTCTGTAAAGCT 481
314 AAGAGCATGCAGAGAAGATTTGTTGTTGGCTCAAGAAGATGGGAGCTGCAACGC 373
482 GGACACCGGACTACTATGGCCAAAGGCTATCTGTTCCTGCCACTACCACTGAGCTCC 541

```

```

Db 374 GGTCTCTCGGACTCACTATGCGCCAGAAAGCAATCTTTGTTTCTCCCCCTCCAGTCTCTTCT 433
Qy 542 GACTAA 547
Db 434 GATTAA 439

RESULT 14
AAQ10399
ID AAQ10399 standard; cDNA; 454 BP.
XX
XX AAQ10399;
AC
XX 25-MAR-2003 (revised)
DT 15-APR-1991 (first entry)
XX
XX Human acidic fibroblast growth factor gene.
DE
XX aFGF; antibody; antigen; cancer; ss.
KW
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 14.442
FT CDS
FT /*tag= a
FT /product= "aFGF"
XX
XX JP02306996-A.
PN
XX
XX 20-DEC-1990.
PD
XX
XX 03-JUL-1989; 89JP-00172542.
PF
XX 04-JUL-1988; 88JP-00166275.
PR
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX WPI; 1991-040150/06.
DR P-PSDB; AAR10527.
DR
XX
XX Anti-acid antibody, for cancer diagnosis, etc. - is obsd. by using
PT complex of partial peptide(s) of acid fibroblast growth factor and
PT protein as antigen.
PT
XX Disclosure; Fig 1; 19pp; Japanese.
PS
XX The sequence can be used to produce recombinant aFGF in plasmid pTB975.
CC Peptides derived from the protein can be used to as antigens to produce
CC anti-aFGF antibodies. The Abs can be used for immunochemically measuring
CC aFGF, and for purifying aFGF. They are useful as reagents in the
CC diagnosis of various cancers or diseases of the CNS. Purified aFGF has
CC wound healing and nerve cell proliferating properties. (Updated on 25-MAR
CC -2003 to correct PA field.)
XX
XX Sequence 454 BP; 127 A; 110 C; 119 G; 98 T; 0 U; 0 Other;
SQ
Query Match 46.0%; Score 290; DB 2; Length 454;
Best Local Similarity 80.0%; Pred. No. 6.7e-68;
Matches 341; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

122 ATGTTTAACTTCGCGCGGAATTACAAAACCCCAAGCTTCTTTACTGAGTAACGGA 181
14 ATGTTTAACTTCGCGCGGAATTACAAAACCCCAAGCTTCTTTACTGAGTAACGGA 73
182 GGACACTTCTCGCAATTCGCCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCGAC 241
74 GGCCACTTCTGAGGATTCCTCCGATGGCACAGTAGATGGGACTCGCGATCGCTCCGAC 133
242 CAGCACATTCAGTGCACACTCTCGCGCGAAGAGCTTGAGAGGCTTATATCAAGTCCGAC 301
134 CAGCACATTCAGTGCACACTCTCGCGCGAAGAGCTTGAGAGGCTTATATCAAGTCCGAC 193
302 GAGACTGGCAGTACCTTGCCATGGACACCGATGGGCTTCTGTATGGCTCACAGACGCT 361

```

Db 194 GAGACTGGCGAGTCTTGGCAATGGACACCGAGGGCTTTTATACGGCTCAGACACCA 253
QY 362 AACGAAGATGCTGTTCTTAGAAGAGACTAGAGAAACCATTTACAACACGTAATATCG 421
Db 254 AATGAGGAATGTTGTTCTGGAAGGCTGGAGGAGAACCAATTACAACACCTATATATCC 313
QY 422 AAAAAACATGCAGAGAGAACTGGTTTGTAGGCCTTAAAAAATGGTTCTGTAAAGGT 481
Db 314 AAGAAGCATGCAGAGAGAAATGGTTTGTGGCCTCAAGAAGAATGGGAGCTGCAACGC 373
QY 482 GGACACGAGCACTACTATGCGCAAGAGGCTATCTTGTCTCCACTACCACTGAGCTCC 541
Db 374 GGTCTCGGACTCACTATGCGCAGAAAGCAATCTTGTCTCCCTGCCAGTCTCTTCT 433
QY 542 GACTAA 547
Db 434 GATTAA 439

RESULT 15
AAQ10166
ID AAQ10166 standard; cDNA; 454 BP.

XX AC AAQ10166;
XX 25-MAR-2003 (revised)
DT 19-MAR-1991 (first entry)
XX Human acidic fibroblast growth factor encoding sequence.
XX aFGF; wound healing; pTB917; ds.
XX Homo sapiens.

XX Key Location/Qualifiers
FT CDS 14..435
FT /*tag= a
XX EP406738-A.
XX 09-JAN-1991.
XX 30-JUN-1990; 90EP-00112532.
XX 03-JUL-1989; 89JP-00172542.
XX 29-SEP-1989; 89JP-00256193.
XX (TAKE) TAKEDA CHEM IND LTD.
XX WPI; 1991-009738/02.

XX Production of acidic FGF protein - using expression vector to transform
PT host cells and express aFGF gene.
XX Disclosure; Fig 1; 23pp; English.
XX Sequence may be used to transform an E.coli expression system, allowing
CC for efficient production of the aFGF, useful in promotion of wound
CC healing. (Updated on 25-MAR-2003 to correct PA field.)
XX Sequence 454 BP; 127 A; 110 C; 119 G; 98 T; 0 U; 0 Other;

Query Match 46.0%; Score 290; DB 2; Length 454;
Best Local Similarity 80.0%; Pred. No. 6.7e-68;
Matches 341; Conservative 0; Mismatches 85; Indels 0; Gaps 0;
QY 122 ATGTTTAACCTTCGCGCGGGAATTACAAAACCCAGCTTCTTACTGCGAGTAACGGA 181
Db 14 ATGTTTAATCTGCTCCCGGGAATTACAAGAGCCCAACTCTCTACTGCGAACCGG 73
QY 182 GGACACTTCTCGGAATCTGCGAGATGGCAGATGAGTGGGACTCGGATCGCTCCGAC 241

Db 74 GGCCACTTCTCGAGATTCTTCCGATGGCACAGTGGATGGGCAAGGACAGGACGAC 133
QY 242 CAGCACATTTAGCTGCAACTCTCGGCGGAAAGCGTTGGAGAGGTCTATATCAAGTCCGACG 301
Db 134 CAGCACATTTAGCTGCAACTCAGTGCAGAAAGCGTGGGGGAGGTGTATATAAGAGTACC 193
QY 302 GAGACTGGCCAGTACCTTGGCATGGACACCGATGGGCTTCTGTATGGCTCACAGACGCT 361
Db 194 GAGACTGGCCAGTACTTGGCAATGGACACCGGCTTTTATACGGCTCACAGACCA 253
QY 362 AACGAAGAATGCTTGTGTTTCTAGAAAGACTAGAAAGAAACCATTTACAACACGTAATATCG 421
Db 254 AATGAGGAATGTTGTTCTTGGAAAGGCTGGAGGAGAACCAATTACAACACCTATATCC 313
QY 422 AAAAAACATGCAGAGAGAACTGGTTTGTAGGCCTTAAAAAATGGTTCTGTAAAGGT 481
Db 314 AAGAAGCATGCAGAGAGAAATGGTTTGTGGCCTCAAGAAGAATGGGAGCTGCAACGC 373
QY 482 GGACACGAGCTCACTATGCGCAGAAAGGCTATCTTGTCTCCACTACCACTGAGCTCC 541
Db 374 GGTCTCGGACTCACTATGCGCAGAAAGCAATCTTGTCTCCCTGCCAGTCTCTTCT 433
QY 542 GACTAA 547
Db 434 GATTAA 439

Search completed: June 17, 2005, 00:49:05
Job time : 480 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 17, 2005, 00:27:22 ; Search time 164 Seconds
(without alignments)
6285.697 Million cell updates/sec

Title: US-10-649-480A-6
Perfect score: 630
Sequence: 1 ggcgtagagatcgagatctc.....ctgagatccggctgctaaca 630

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	630	100.0	630	4	US-09-929-945-6
2	630	100.0	630	4	US-09-929-918-6
3	584	92.7	630	4	US-09-929-945-4
4	584	92.7	630	4	US-09-929-918-4
5	567.4	90.1	990	4	US-09-929-918-10
6	536	85.1	630	4	US-09-929-945-1
7	536	85.1	630	4	US-09-929-918-1
8	341.6	54.2	8501	3	US-08-793-900-1
9	290	46.0	454	6	5175147-1
10	290	46.0	454	6	5175147-1
11	285.4	45.3	490	4	US-09-023-655-1390
12	285.4	45.3	638	3	US-09-098-628-3
13	284	45.1	468	4	US-09-929-945-3
14	284	45.1	468	4	US-09-929-918-3
15	242	38.4	450	6	5437995-1
16	242	38.4	450	6	5437995-1
17	221.8	35.2	454	3	US-09-030-613-14
18	221.8	35.2	454	3	US-09-451-905-14
19	141.6	22.5	261	1	US-08-070-165F-1
20	141.6	22.5	261	2	US-08-885-418-1
21	141.6	22.5	477	1	US-08-230-373B-16
22	131.4	20.9	483	3	US-09-220-077C-1
23	131.4	20.9	483	4	US-09-826-210A-1
24	131.4	20.9	483	4	US-09-722-495A-1
25	128	20.3	442	3	US-09-385-114-1
26	128	20.3	442	3	US-09-417-721-4
27	125.6	19.9	5443	2	US-08-929-967-1

c	28	125.2	19.9	6361	3	US-08-646-538-7	Sequence 7, Appli
c	29	125.2	19.9	6361	3	US-09-503-222-7	Sequence 7, Appli
	30	124.4	19.7	3572	3	US-09-072-596-337	Sequence 337, App
	31	124.4	19.7	3572	3	US-09-072-967-342	Sequence 342, App
	32	124.4	19.7	7676	3	US-09-056-556-213	Sequence 213, App
	33	124.4	19.7	7676	3	US-09-072-596-208	Sequence 208, App
	34	124.4	19.7	7676	4	US-09-072-967-213	Sequence 9, Appli
	35	124.4	19.7	7676	4	US-09-287-849-9	Sequence 1, Appli
	36	124	19.7	1010	3	US-09-070-408-1	Sequence 1, Appli
	37	124	19.7	5502	4	US-09-702-705-785	Sequence 785, App
	38	124	19.7	5502	4	US-09-736-457-785	Sequence 785, App
	39	124	19.7	5502	4	US-09-614-124B-785	Sequence 785, App
	40	124	19.7	5502	4	US-09-671-325-785	Sequence 785, App
	41	124	19.7	5502	4	US-09-589-184-785	Sequence 785, App
	42	124	19.7	5502	4	US-09-658-824-785	Sequence 785, App
	43	124	19.7	6353	4	US-09-702-705-784	Sequence 784, App
	44	124	19.7	6353	4	US-09-736-457-784	Sequence 784, App
	45	124	19.7	6353	4	US-09-614-124B-784	Sequence 784, App

ALIGNMENTS

RESULT 1
US-09-929-945-6
; Sequence 6, Application US/09929945
; Patent No. 6642026
; GENERAL INFORMATION:
; APPLICANT: Stegmann, Thomas
; APPLICANT: Kordyum, Vitaliy A.
; APPLICANT: Chernykh, Svitlana I.
; APPLICANT: Slavchenko, Iryna Yu.
; APPLICANT: Vozianov, Oleksandr
; TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT
; FILE REFERENCE: CVGENG.008A
; CURRENT APPLICATION NUMBER: US/09/929,945
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized sequence for human acidic
; OTHER INFORMATION: Fibroblast Growth Factor (140 amino acids) using
; OTHER INFORMATION: preferred codons for E. coli
; NAME/KEY: CDS
; LOCATION: (122)...(544)
US-09-929-945-6

Query Match	100.0%;	Score 630;	DB 4;	Length 630;
Best Local Similarity	100.0%;	Pred. No. 1e-183;		
Matches 630;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	GCCTAGAGGTCGAGATCTCGATCCCGCGAAATTAATACGACTCCTATAGGGGAATTGT	60	
Db	1	GCCTAGAGGTCGAGATCTCGATCCCGCGAAATTAATACGACTCCTATAGGGGAATTGT	60	
Qy	61	GACGGGATACAAATTCCTCTAGAAATATTTTGTAACTTTAAGAGGAGATATACA	120	
Db	61	GACGGGATACAAATTCCTCTAGAAATATTTTGTAACTTTAAGAGGAGATATACA	120	
Qy	121	TATGTTTAACTTCCTCCGCGGGAATTAACAAAAACCAAGCTTTCTTCTGCGAGTAACGG	180	
Db	121	TATGTTTAACTTCCTCCGCGGGAATTAACAAAAACCAAGCTTTCTTCTGCGAGTAACGG	180	
Qy	181	AGACACTTCCTCGGAATTCCTCCAGATGCGACAGTAGATGGGACTCCGATCCCTCCGA	240	
Db	181	AGACACTTCCTCGGAATTCCTCCAGATGCGACAGTAGATGGGACTCCGATCCCTCCGA	240	
Qy	241	CCAGCACATTGCTGCAACTCTCTCGGCGAAAGCTTTGGAGAGGTCTTATATCAAGTCGAC	300	

Db	241		CCAGCACATTCAAGTCGAACCTCTCGGCCGAAGCGTTGGAGAGGCTCTATATCAAGTCGAC	300
Qy	301		GGAGACTGCGCCAGTAGTACCTTGGCCATGGACACCGATGGGCTTCTGTATGGCTCAGACAGCGC	360
Db	301		GGAGACTGCGCCAGTAGTACCTTGGCCATGGACACCGATGGGCTTCTGTATGGCTCAGACAGCGC	360
Qy	361		TACGGAAGAATCGTTGTTTCTTAGAAGACTAGAGAAGAAACCATTTACAACACGTACATATC	420
Db	361		TACGGAAGAATCGTTGTTTCTTAGAAGACTAGAGAAGAAACCATTTACAACACGTACATATC	420
Qy	421		GAAGAAACATGCAGAGAGAACTGGTTGTTAGGCGCTTAAAAAAATGGTTCCTGTAAAGCG	480
Db	421		GAAGAAACATGCAGAGAGAACTGGTTGTTAGGCGCTTAAAAAAATGGTTCCTGTAAAGCG	480
Qy	481		TGGACCACGAGCTCACTATGGCCAAAAGGCTATCTTGTTCCTGCACATACAGTGAAGCTC	540
Db	481		TGGACCACGAGCTCACTATGGCCAAAAGGCTATCTTGTTCCTGCACATACAGTGAAGCTC	540
Qy	541		CGACTAAGGATCCGAATTCGAGCTCCGTCGACAAAGCTTGGCGCGGCACTCGAGCACACC	600
Db	541		CGACTAAGGATCCGAATTCGAGCTCCGTCGACAAAGCTTGGCGCGGCACTCGAGCACACC	600
Qy	601		ACCACACCACTGAGATCCGGCTGCTAAACA	630
Db	601		ACCACACCACTGAGATCCGGCTGCTAAACA	630

```

RESULT 2
US-09-929-918-6
; Sequence 6, Application US/09929918
; Patent No. 6773899
; GENERAL INFORMATION:
; APPLICANT: Kordyum, Vitaliy A.
; APPLICANT: Chernykh, Svitlana I.
; APPLICANT: Slavchenko, Iryna Yu.
; APPLICANT: Vozitanov, Oleksandr
; TITLE OF INVENTION: PHAGE-DEPENDENT SUPER PRODUCTION OF
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN AND PEPTIDES
; FILE REFERENCE: PHAGE.006A
; CURRENT APPLICATION NUMBER: US/09/929,918
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 09/318,288
; PRIOR FILING DATE: 1993-05-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This sequence is a chemically synthesized sequence
; OTHER INFORMATION: encoding a 140 amino acid form of fibroblast
; OTHER INFORMATION: growth factor with alterations for preferred codon
; OTHER INFORMATION: usage in E. coli
; NAME/KEY: CDS
; LOCATION: (122)...(544)
US-09-929-918-6

```

121	TATGTTTAACTTCCGCCCGGGAAATACAAAAAACCCCAAGCTTCTTTTACTCGAGTAAACGG	180
181	AGGACACTTCTCTGCGAAATCTCGCCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCGA	240
181	AGGACACTTCTCTGCGAAATCTCGCCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCGA	240
241	CGAGCAATTTCAGTGTGCAACTCTCTCGGCCGAAAGCGTTGGAGAGGTCTATATCAAGTCGAC	300
241	CGAGCAATTTCAGTGTGCAACTCTCTCGGCCGAAAGCGTTGGAGAGGTCTATATCAAGTCGAC	300
301	GGAGACTGGCCAGTACCTTGGCATGGACACCGATGGGCTTCTGTATGGCTCACACAGCGCC	360
301	GGAGACTGGCCAGTACCTTGGCATGGACACCGATGGGCTTCTGTATGGCTCACACAGCGCC	360
361	TACGAAAGAAATGCTGTGTTTCTAGAAAGACTAGAGAAACCAATTACACAGTGATCATATC	420
361	TACGAAAGAAATGCTGTGTTTCTAGAAAGACTAGAGAAACCAATTACACAGTGATCATATC	420
421	GAAAAACATGTCAGAGAAGAACTGGTTTGTAGGCTTAAAAAAAATGGTTCTGTGAAGCG	480
421	GAAAAACATGTCAGAGAAGAACTGGTTTGTAGGCTTAAAAAAAATGGTTCTGTGAAGCG	480
481	TGGACCAACGAGTCACTATATGGCCAAAAGGCTATCTTGTTCTGGCACTACCAAGTGAGTTC	540
481	TGGACCAACGAGTCACTATATGGCCAAAAGGCTATCTTGTTCTGGCACTACCAAGTGAGTTC	540
541	CGACTAAGGATCCGAAATTCGAGTCCCGTCGACAAGCTTGGCGCCGCACTTCGAGCACCAACC	600
541	CGACTAAGGATCCGAAATTCGAGTCCCGTCGACAAGCTTGGCGCCGCACTTCGAGCACCAACC	600
601	ACCACCAACCACTGAGATCCGCGTCTCTAAAC	630
601	ACCACCAACCACTGAGATCCGCGTCTCTAAAC	630

```

RESULT 3
US-09-929-945-4
; Sequence 4, Application US/09929945
; Patent No. 6642026
; GENERAL INFORMATION:
; APPLICANT: Stegmann, Thomas
; APPLICANT: Kordyum, Vitaliy A.
; APPLICANT: Chernykh, Svitlana I.
; APPLICANT: Slavchenko, Iryna Yu.
; APPLICANT: Vozianov, Oleksandr
; TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR 155
; FILE REFERENCE: CVGENG.008A
; CURRENT APPLICATION NUMBER: US/09/929,945
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized sequence for human acidic
; OTHER INFORMATION: Fibroblast Growth Factor (134 amino acids) using
; OTHER INFORMATION: preferred codons for E. coli
; NAME/KEY: CDS
; LOCATION: (122)...(526)
; US-09-929-945-4

```

Query Match	92.7%	Score 584;	DB 4;	Length 630;
Best Local Similarity	97.1%	Pred. No. 1.5e-169;		
Matches 612;	Conservative 0;	Mismatches 0;	Indels 18;	Gaps 1
Qy	1	GCCTAGAGGATCGAGATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGGAATTGT		60
Db	1	GCCTAGAGGATCGAGATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGGAATTGT		60
Qy	61	GAGCGGATAACAATTCCCTCTAGAAATAATTTTGTTTAACTTTAAGAAGAGAGATATACA		120

```
Db 61 GAGCGGATACAAATCCCTCTAGAAATAATTTGTTAACTTTAAGAGGAGATATACA 120
Qy 121 TATGTTTAACTTCGCGCGCGGAAATTAACAAAACCCAGAGCTTCTTACTGAGTAAAGG 180
Db 121 TAT-----GAAATTAACAAAACCCAGAGCTTCTTACTGAGTAAAGG 162
Qy 181 AGGACACTTCTCGGAATTCGCCAGATGGCACAGTATGGGACTCGCGATCGCTCCGA 240
Db 163 AGGACACTTCTCGGAATTCGCCAGATGGCACAGTATGGGACTCGCGATCGCTCCGA 222
Qy 241 CCAGCACATTACGCTGCAACTCTCGGCGGAAAGCGTTGGAGAGGTCCTATATCAAGTCGAC 300
Db 223 CCAGCACATTACGCTGCAACTCTCGGCGGAAAGCGTTGGAGAGGTCCTATATCAAGTCGAC 282
Qy 301 GGAGACTGCCAGTACCTTGGCATGACACCGATGGGCTTCTGTATGGCTACACAGCGCC 360
Db 283 GGAGACTGCCAGTACCTTGGCATGACACCGATGGGCTTCTGTATGGCTACACAGCGCC 342
Qy 361 TAACGAGAGATGCTTGTCTAGAAAGACTAGAAAGAAACCAATTACACACGTACATATC 420
Db 343 TAACGAGAGATGCTTGTCTAGAAAGACTAGAAAGAAACCAATTACACACGTACATATC 402
Qy 421 GAAAAAACAATGAGAGAACTGGTTTGTAGAGCCTTAAAAAAATGGTTCTCTGTAAGCG 480
Db 403 GAAAAAACAATGAGAGAACTGGTTTGTAGAGCCTTAAAAAAATGGTTCTCTGTAAGCG 462
Qy 481 TGGACACCGAGTCACTATGGCCAAAAGGCTATCTTGTCTGCCACTACCAAGTGAAGTC 540
Db 463 TGGACACCGAGTCACTATGGCCAAAAGGCTATCTTGTCTGCCACTACCAAGTGAAGTC 522
Qy 541 CGACTAAGGATCGAATTCGAGCTCCGTCGACAAAGCTTGGGCGCGCACTCGAGCACACC 600
Db 523 CGACTAAGGATCGAATTCGAGCTCCGTCGACAAAGCTTGGGCGCGCACTCGAGCACACC 582
```

RESULT 4

```
US-09-929-918-4
; Sequence 4, Application US/09929918
; Patent No. 6773899
; GENERAL INFORMATION:
; APPLICANT: Kordyum, Vitaliy A.
; APPLICANT: Chernykh, Svitlana I.
; APPLICANT: Slavchenko, Iryna Yu.
; APPLICANT: Vozianov, Oleksandr
; TITLE OF INVENTION: PHAGE-DEPENDENT SUPER PRODUCTION OF
; FILE REFERENCE: PHAGE.006A
; CURRENT APPLICATION NUMBER: US/09/929,918
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 09/318,288
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This sequence is a chemically synthesized sequence
; OTHER INFORMATION: encoding a 134 amino acid form of fibroblast
; OTHER INFORMATION: growth factor with alterations for preferred codon
; OTHER INFORMATION: usage in E. coli
; NAME/KEY: CDS
; LOCATION: (122)...(526)
US-09-929-918-4
```

Query Match 92.7%; Score 584; DB 4; Length 630;
Best Local Similarity 97.1%; Pred. No. 1.5e-169;

```
Matches 612; Conservative 0; Mismatches 0; Indels 18; Gaps 1;
Qy 1 GCGTAGAGGATCGAGATCTCGATCCCGGAAATTAATACGACTCACTATAGGGGAATGT 60
Db 1 GCGTAGAGGATCGAGATCTCGATCCCGGAAATTAATACGACTCACTATAGGGGAATGT 60
Qy 61 GAGCGGATACAAATTCCTCTAGAAATAATTTGTTTAACTTTAAGAGGAGATATACA 120
Db 61 GAGCGGATACAAATTCCTCTAGAAATAATTTGTTTAACTTTAAGAGGAGATATACA 120
Qy 121 TATGTTTAACTTCGCGCGCGGAAATTAACAAAACCCAGAGCTTCTTACTGAGTAAAGG 180
Db 121 TAT-----GAAATTAACAAAACCCAGAGCTTCTTACTGAGTAAAGG 162
Qy 181 AGGACACTTCTCGGAATTCGCCAGATGGCACAGTATGGGACTCGCGATCGCTCCGA 240
Db 163 AGGACACTTCTCGGAATTCGCCAGATGGCACAGTATGGGACTCGCGATCGCTCCGA 222
Qy 241 CCAGCACATTACGCTGCAACTCTCGGCGGAAAGCGTTGGAGAGGTCCTATATCAAGTCGAC 300
Db 223 CCAGCACATTACGCTGCAACTCTCGGCGGAAAGCGTTGGAGAGGTCCTATATCAAGTCGAC 282
Qy 301 GGAGACTGCCAGTACCTTGGCATGACACCGATGGGCTTCTGTATGGCTACACAGCGCC 360
Db 283 GGAGACTGCCAGTACCTTGGCATGACACCGATGGGCTTCTGTATGGCTACACAGCGCC 342
Qy 361 TAACGAGAGATGCTTGTCTAGAAAGACTAGAAAGAAACCAATTACACACGTACATATC 420
Db 343 TAACGAGAGATGCTTGTCTAGAAAGACTAGAAAGAAACCAATTACACACGTACATATC 402
Qy 421 GAAAAAACAATGAGAGAACTGGTTTGTAGAGCCTTAAAAAAATGGTTCTCTGTAAGCG 480
Db 403 GAAAAAACAATGAGAGAACTGGTTTGTAGAGCCTTAAAAAAATGGTTCTCTGTAAGCG 462
Qy 481 TGGACACCGAGTCACTATGGCCAAAAGGCTATCTTGTCTGCCACTACCAAGTGAAGTC 540
Db 463 TGGACACCGAGTCACTATGGCCAAAAGGCTATCTTGTCTGCCACTACCAAGTGAAGTC 522
Qy 541 CGACTAAGGATCGAATTCGAGCTCCGTCGACAAAGCTTGGGCGCGCACTCGAGCACACC 600
Db 523 CGACTAAGGATCGAATTCGAGCTCCGTCGACAAAGCTTGGGCGCGCACTCGAGCACACC 582
Qy 601 ACCACCACTGAGATCCGGCTGCTAACA 630
Db 583 ACCACCACTGAGATCCGGCTGCTAACA 612
```

RESULT 5

```
US-09-929-918-10
; Sequence 10, Application US/09929918
; Patent No. 6773899
; GENERAL INFORMATION:
; APPLICANT: Kordyum, Vitaliy A.
; APPLICANT: Chernykh, Svitlana I.
; APPLICANT: Slavchenko, Iryna Yu.
; APPLICANT: Vozianov, Oleksandr
; TITLE OF INVENTION: PHAGE-DEPENDENT SUPER PRODUCTION OF
; FILE REFERENCE: PHAGE.006A
; CURRENT APPLICATION NUMBER: US/09/929,918
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 09/318,288
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 990
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized sequence for human
; OTHER INFORMATION: interferon alpha- 2b
; NAME/KEY: promoter
```

; LOCATION: (231)...(249)
; NAME/KEY: CDS
; LOCATION: (320)...(784)
US-09-929-918-10

Query Match 90.1%; Score 567.4; DB 4; Length 990;
Best Local Similarity 92.8%; Pred. No. 2.4e-164;
Matches 623; Conservative 0; Mismatches 6; Indels 42; Gaps 1;

```

QY 2 CCGTAGAGGATCCGAGATCTCGATCCCGCGAAATTAATACGACTCATATAGGGGAATTGTG 61
Db 200 CGTGGGGCGCGAGATCTCGATCCCGCGAAATTAATACGACTCATATAGGGGAATTGTG 259

QY 62 ACGGATACAAATCCCTCTAGAAATTAATTTGTTAACTTTAAGAGGAGATATACAT 121
Db 260 ACGGATACAAATCCCTCTAGAAATTAATTTGTTAACTTTAAGAGGAGATATACAT 319

QY 122 ATG-----TTTAACTTCCGCC 139
Db 320 ATGGCTGAAGGGGAATACACCCTTTACAGCGTTAAACGAGAAATTTAACTTCCGCC 379

QY 140 GGGAAATTACAAAAACCAAGCTCTTTACTGCAAGTAACGAGGACACTTCTCGGAATT 199
Db 380 GGGAAATTACAAAAACCAAGCTCTTTACTGCAAGTAACGAGGACACTTCTCGGAATT 439

QY 200 CTGCCAGATGGCAGTACGATGGGACTCGGATCGCTCCGACGACACATTCAGCTGCA 259
Db 440 CTGCCAGATGGCAGTACGATGGGACTCGGATCGCTCCGACGACACATTCAGCTGCA 499

QY 260 CTCTGGCCGGAAGCGTTGGAGAGGTCTATATCAAGTCGACGAGACTGGCCAGTACCTT 319
Db 500 CTCTGGCCGGAAGCGTTGGAGAGGTCTATATCAAGTCGACGAGACTGGCCAGTACCTT 559

QY 320 GCATGGACACCGATGGGCTTCTGTATGCTCAGACGCTTACGAGAAATGCTTGT 379
Db 560 GCATGGACACCGATGGGCTTCTGTATGCTCAGACGCTTACGAGAAATGCTTGT 619

QY 380 CTAGAAGACTAGAGAAACCAATTAACACGATACATATCGAAAAACATCGAGAG 439
Db 620 CTAGAAGACTAGAGAAACCAATTAACACGATACATATCGAAAAACATCGAGAG 679

QY 440 AACTGGTTGTAGGCTTAAAAAATGTTCTCTGAAGCGTGGACCGGACTCACTAT 499
Db 680 AACTGGTTGTAGGCTTAAAAAATGTTCTCTGAAGCGTGGACCGGACTCACTAT 739

QY 500 GGCCTGAGGCTATCTTGTCTGCGCACTACAGTGAGCTCCGACTAAGGATCCGAATTC 559
Db 740 GGCCTGAGGCTATCTTGTCTGCGCACTACAGTGAGCTCCGACTAAGGATCCGAATTC 799

QY 560 GAGCTCCGTCGACAGCTTGGCGCGCACTCGAGCACCACGACCACTGAGATCC 619
Db 800 GAGCTCCGTCGACAGCTTGGCGCGCACTCGAGCACCACGACCACTGAGATCC 859

QY 620 GCGTCTAACA 630
Db 860 GCGTCTAACA 870

```

RESULT 6
US-09-929-945-1
; Sequence 1, Application US/09929945
; Patent No. 6642026
; GENERAL INFORMATION:
; APPLICANT: Stegmann, Thomas
; APPLICANT: Kordyum, Vitaliy A.
; APPLICANT: Chernykh, Svitlana I.
; APPLICANT: Slavchenko, Iryna Yu.
; APPLICANT: Vozianov, Olexandr
; TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT
; FILE REFERENCE: CDS/ENG.008A
; CURRENT APPLICATION NUMBER: US/09/929,945
; CURRENT FILING DATE: 2001-08-15

; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized sequence for human acidic
; OTHER INFORMATION: Fibroblast Growth Factor (155 amino acids) using
; NAME/KEY: CDS
; LOCATION: (122)...(590)
US-09-929-945-1

Query Match 85.1%; Score 536; DB 4; Length 630;
Best Local Similarity 93.3%; Pred. No. 9e-155;
Matches 588; Conservative 0; Mismatches 0; Indels 42; Gaps 1;

```

QY 1 CGGTAGAGGATCGAGATCTCGATCCCGCGAAATTAATACGACTCATATAGGGGAATTGT 60
Db 1 CGGTAGAGGATCGAGATCTCGATCCCGCGAAATTAATACGACTCATATAGGGGAATTGT 60

QY 61 GAGCGGATACAAATCCCTCTAGAAATTAATTTGTTAACTTTAAGAGGAGATATACA 120
Db 61 GAGCGGATACAAATCCCTCTAGAAATTAATTTGTTAACTTTAAGAGGAGATATACA 120

QY 121 TATG-----TTTAACTTCCGCC 138
Db 121 TATGGCTGAAGGGGAATACACCCTTTACAGCGTTAAACGAGAAATTTAACTTCCGCC 180

QY 139 CGGGAATTTACAAAAACCAAGCTTCTTACTGCAAGTAACGAGGACACTTCTCGGAAT 198
Db 181 CGGGAATTTACAAAAACCAAGCTTCTTACTGCAAGTAACGAGGACACTTCTCGGAAT 240

QY 199 TCTGCAGATGGCAGTAGATGGGACTCGGATCGCTCCGACGAGACTGGCCAGTACCT 258
Db 241 TCTGCAGATGGCAGTAGATGGGACTCGGATCGCTCCGACGAGACTGGCCAGTACCT 300

QY 259 ACTCTCGGCCGAAACGTTGGAGAGGTCTATATCAAGTCGACGAGACTGGCCAGTACCT 318
Db 301 ACTCTCGGCCGAAACGTTGGAGAGGTCTATATCAAGTCGACGAGACTGGCCAGTACCT 360

QY 319 TGCCATGACACCGATGGCTTCTGTATGCTCAGACGCTTACGAGAAATGCTTGT 378
Db 361 TGCCATGACACCGATGGCTTCTGTATGCTCAGACGCTTACGAGAAATGCTTGT 420

QY 379 TCTAGAAGACTAGAGAAACCAATTAACACGATACATATCGAAAAACATCGAGAGAA 438
Db 421 TCTAGAAGACTAGAGAAACCAATTAACACGATACATATCGAAAAACATCGAGAGAA 480

QY 439 GAATGGTTTGTAGGCTTAAAAAATGTTCTCTGAAGCGTGGACCACTGAGTCACTA 498
Db 481 GAATGGTTTGTAGGCTTAAAAAATGTTCTCTGAAGCGTGGACCACTGAGTCACTA 540

QY 499 TGCCCAAAAGGCTATCTTGTCTCGCACTTACGAGTGGCTCCGACTAAGGATCCGAAT 558
Db 541 TGCCCAAAAGGCTATCTTGTCTCGCACTTACGAGTGGCTCCGACTAAGGATCCGAAT 600

QY 559 CGAGCTCCGTCGACAGCTTGGCGCGCAC 588
Db 601 CGAGCTCCGTCGACAGCTTGGCGCGCAC 630

```

RESULT 7
US-09-929-918-1
; Sequence 1, Application US/09929918
; Patent No. 6773899
; GENERAL INFORMATION:
; APPLICANT: Kordyum, Vitaliy A.
; APPLICANT: Chernykh, Svitlana I.
; APPLICANT: Slavchenko, Iryna Yu.
; APPLICANT: Vozianov, Olexandr
; TITLE OF INVENTION: PHAGE-DEPENDENT SUPER PRODUCTION OF

; TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN AND PEPTIDES
; FILE REFERENCE: PHAGE 006A
; CURRENT APPLICATION NUMBER: US/09/929,918
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 09/318,288
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This sequence was chemically synthesized based
; OTHER INFORMATION: upon the amino acid sequence of human acidic
; OTHER INFORMATION: fibroblast growth factor (155 amino acids) using
; OTHER INFORMATION: codons which are used in highly expressed proteins from E. coli.
; NAME/KEY: CDS
; LOCATION: (122)...(590)
; US-09-929-918-1
;
Query Match 85.1%; Score 536; DB 4; Length 630;
Best Local Similarity 93.3%; Pred. No. 9e-155;
Matches 588; Conservative 0; Mismatches 0; Indels 42; Gaps 1;
;
QY 1 GCCTAGGATCGAGATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGGAATTGT 60
DB 1 GCCTAGGATCGAGATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGGAATTGT 60
;
QY 61 GACGGATACAAATTCCTCTAGAATAATTTTGTAACTTTAAGAAGGAGATATACA 120
DB 61 GACGGATACAAATTCCTCTAGAATAATTTTGTAACTTTAAGAAGGAGATATACA 120
;
QY 121 TATG-----TTTAACTTCGGCC 138
DB 121 TATGGCTGAAGGGGAATACCACTTTACAGCGTTTAAACGGGAAATTTAACTTCGGCC 180
;
QY 139 CGGGAATTACAAAACCCCAAGCTTCTTTACTCGAGTAAACGGAGGACACTTCTCGGAAT 198
DB 181 CGGGAATTACAAAACCCCAAGCTTCTTTACTCGAGTAAACGGAGGACACTTCTCGGAAT 240
;
QY 199 TCTGCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCGACCGACACATTCAGCTGCA 258
DB 241 TCTGCCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCGACCGACACATTCAGCTGCA 300
;
QY 259 ACTCTCGGCCGAAAGCTTGGAGAGTCTATATCAAGTCGACGGAGACTGGCCAGTACCT 318
DB 301 ACTCTCGGCCGAAAGCTTGGAGAGTCTATATCAAGTCGACGGAGACTGGCCAGTACCT 360
;
QY 319 TGCATGACACCGATGGCTTCTGTATGGCTACAGACCGCTTAAACGAAGATGCTTGT 378
DB 361 TGCATGACACCGATGGCTTCTGTATGGCTACAGACCGCTTAAACGAAGATGCTTGT 420
;
QY 379 TCTAGAAGACTAGAAGAAACCAATTACACAGCTCATATCGAAAAACATGCAGAGAA 438
DB 421 TCTAGAAGACTAGAAGAAACCAATTACACAGCTCATATCGAAAAACATGCAGAGAA 480
;
QY 439 GAATCGTTTGTAGGCCCTTAAAAAATGGTTCTGTAAAGGTGGACCAAGGACTCACTA 498
DB 481 GAATCGTTTGTAGGCCCTTAAAAAATGGTTCTGTAAAGGTGGACCAAGGACTCACTA 540
;
QY 499 TGGCAAAAGCTATCTGTTCCTGCCACTACGATGAGCTCCGACTAAGGATCCGAATT 558
DB 541 TGGCAAAAGCTATCTGTTCCTGCCACTACGATGAGCTCCGACTAAGGATCCGAATT 600
;
QY 559 CGAGCTCGTCGACAAGCTTCGGCCGCGAC 588
DB 601 CGAGCTCGTCGACAAGCTTCGGCCGCGAC 630
;

; Patent No. 6143518
; GENERAL INFORMATION:
; APPLICANT: CAMERON, Beatrice
; APPLICANT: CROUZET, Joel
; TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF RECOMBINANT
; TITLE OF INVENTION: PROTEINS, PLASMIDS AND MODIFIED CELLS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,900
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01178
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: FR 94/11049
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky Esq., Martin F.
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: ST94069-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3816
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8501 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cdna
; US-08-793-900-1
;
Query Match 54.2%; Score 341.6; DB 3; Length 8501;
Best Local Similarity 77.3%; Pred. No. 2.4e-94;
Matches 447; Conservative 0; Mismatches 89; Indels 42; Gaps 1;
;
QY 15 GATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGGAATTGTGAGCGGATAACAAT 74
DB 1 GATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGGAATTGTGAGCGGATAACAAT 60
;
QY 75 TCCCTCTAGAAATAATTTTGTAACTTTAAGAAGGAGATATACATAT----- 123
DB 61 TCCCTCTAGAAATAATTTTGTAACTTTAAGAAGGAGATATACATATCGCTGAAGGGG 120
;
QY 124 -----GTTTAACTTCCCGCGGAAATTACAAA 152
DB 121 AAATCAACCTTCACAGCCCTACCGAGAGTTTAACTTCGCTCCAGGAAATTACAGA 180
;
QY 153 AACCAAGCTCTTTTACTGCAGTAACGGAGGACACTTCTTCGGAATTCGCCAGATGGCA 212
DB 181 AGCCCAACTCTCTACTGTAGCAACGGGGGCCACTTCTCTGAGATCCTTCGCGATGGCA 240
;
QY 213 CAGTAGATGGGAATTCGGATCGCTCCGACGAGACATTTCAGCTGCAACTCTCGGCCGAAA 272
DB 241 CAGTGGATGGGACAAAGGGAACAGGAGCAGCAGACATTCAGCTCAGCTCAGTCGCGAAA 300
;
QY 273 GCGTTGGAGAGTCTATATCAAGTCGACGGAGACTGCCAGTACCTTGCATGGACACCG 332
DB 301 GCGTGGGGAGGTGTATATAAGAGATACCGAGACTGCCAGTACTTGGCCNATGGACACCG 360
;
QY 333 ATGGGCTTCTGTATGGCTCACAGACGCTTAACGAAGATGCTTTTCTAGAAAGACTAG 392
;


```

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1390:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 490 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: G396163
; US-09-023-655-1390

```

```

Query Match      45.3%; Score 285.4; DB 4; Length 490;
Best Local Similarity 78.9%; Pred. No. 1.1e-77;
Matches 340; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 120 ATATGTTTAACTTCCGCGGGAATTTACAAAACCCAGCTCTTTTACTGCAGTAACG 179
DB 51 AGAAGTTTAACTTCCGCGGGAATTTACAAAACCCAGCTCTTTTACTGCAGTAACG 110

QY 180 GAGGACACTTCTCGGGAATTTCTCCAGATGGCACAGTAGATGGGACTTCGCGATCGCTCCG 239
DB 111 GGGGCCACTTCTCGGGAATTTCTCCAGATGGCACAGTAGATGGGACTTCGCGATCGCTCCG 170

QY 240 ACCAGCACATTCAGTGCACACTCTCGGCGGAAAGCGTTGGAGAGGCTTATATCAAGTCGA 299
DB 171 ACCAGCACATTCAGTGCACACTCTCGGCGGAAAGCGTTGGAGAGGCTTATATCAAGTCGA 230

QY 300 CGGAGACTGGCCAGTACCTTGCATGACACCGATGGCTTCTGTATGGCTTCACAGACG 359
DB 231 CGGAGACTGGCCAGTACCTTGCATGACACCGATGGCTTCTGTATGGCTTCACAGACG 290

QY 360 CTAAAGGAAGTCTGTTTCTAGAAAGACTAGAAAGAAACCAATTAACAACACGTACATAT 419
DB 291 CAATGAGGAATGTTTGTCTGGAAGGCTGGAGGAGACCATTAACAACACGTACATAT 350

QY 420 CGAAAAAATGCAGAGAAAGAACTGGTTTGTAGGCTTTAAAAAATGGTTCTCTGTAAGC 479
DB 351 CCAAGAGCATGCAGAGAAAGAACTGGTTTGTAGGCTTTAAAAAATGGTTCTCTGTAAGC 410

QY 480 GTGACACCGACTCATTATGGCCAAAGGCTATCTTGTCTTCCCTGACCTACCGAGT 539
DB 411 GCGGTCTCGGACTCATTATGGCCAAAGGCTATCTTGTCTTCCCTGACCTACCGAGT 470

QY 540 CCGACTAAGGA 550
DB 471 CTGATTAAAGA 481

```

```

RESULT 12
US-09-098-628-3
; Sequence 3, Application US/09098628
; Patent No. 6294359
; GENERAL INFORMATION:
; APPLICANT: FIDDES, J.C.
; APPLICANT: ABRAHAM, J.D.
; TITLE OF INVENTION: HUMAN BASIC FIBROBLAST GROWTH
; TITLE OF INVENTION: FACTOR ANALOG

```

```

; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSER: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/098,628
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 21900-20089.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 638 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 91...555
; OTHER INFORMATION:
; US-09-098-628-3

```

```

Query Match      45.3%; Score 285.4; DB 3; Length 638;
Best Local Similarity 78.9%; Pred. No. 1.3e-77;
Matches 340; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 120 ATATGTTTAACTTCCGCGGGAATTTACAAAACCCAGCTCTTTTACTGCAGTAACG 179
DB 131 AGAAGTTTAACTTCCGCGGGAATTTACAAAACCCAGCTCTTTTACTGCAGTAACG 190

QY 180 GAGGACACTTCTCGGGAATTTCTCCAGATGGCACAGTAGATGGGACTTCGCGATCGCTCCG 239
DB 191 GGGGCCACTTCTCGGGAATTTCTCCAGATGGCACAGTAGATGGGACTTCGCGATCGCTCCG 250

QY 240 ACCAGCACATTCAGTGCACACTCTCGGCGGAAAGCGTTGGAGAGGCTTATATCAAGTCGA 299
DB 251 ACCAGCACATTCAGTGCACACTCTCGGCGGAAAGCGTTGGAGAGGCTTATATCAAGTCGA 310

QY 300 CGGAGACTGGCCAGTACCTTGCATGACACCGATGGCTTCTGTATGGCTTCACAGACG 359
DB 311 CGGAGACTGGCCAGTACCTTGCATGACACCGATGGCTTCTGTATGGCTTCACAGACG 370

QY 360 CTAAAGGAAGTCTGTTTCTAGAAAGACTAGAAAGAAACCAATTAACAACACGTACATAT 419
DB 371 CAATGAGGAATGTTTGTCTGGAAGGCTGGAGGAGACCATTAACAACACGTACATAT 430

QY 420 CGAAAAAATGCAGAGAAAGAACTGGTTTGTAGGCTTTAAAAAATGGTTCTCTGTAAGC 479
DB 431 CCAAGAGCATGCAGAGAAAGAACTGGTTTGTAGGCTTTAAAAAATGGTTCTCTGTAAGC 490

QY 480 GTGACACCGACTCATTATGGCCAAAGGCTATCTTGTCTTCCCTGACCTACCGAGT 539
DB 491 GCGGTCTCGGACTCATTATGGCCAAAGGCTATCTTGTCTTCCCTGACCTACCGAGT 550

```

QY 540 CCGACTAAGGA 550
Db 551 CTGATTAAAGA 561

RESULT 13

US-09-929-945-3

; Sequence 3, Application US/09929945
; Patent No. 6642026
; GENERAL INFORMATION:
; APPLICANT: Stegmann, Thomas
; APPLICANT: Kordyum, Vitaliy A.
; APPLICANT: Chernykh, Svitlana I.
; APPLICANT: Slavchenko, Iryna Yu.
; APPLICANT: Vozianov, Oleksandr
; TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT
; FILE REFERENCE: FIBROBLAST GROWTH FACTOR 155
; CURRENT APPLICATION NUMBER: US/09/929,945
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-929-945-3

Query Match 45.1%; Score 284; DB 4; Length 468;

Best Local Similarity 79.0%; Pred. No. 3e-77;
Matches 338; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 120 ATATGTTTAACTTCGGCCCGGAATTACAAAAACCCAAAGTCTCTTACTCGAGTAACG 179

Db 41 AGAAGTTTAACTTCGCTCCAGGGAATTACAGAAGCCCAAACTCTCTACTGTAGCAACG 100

QY 180 GAGGACATCTCCGGAATTCGCCAGATGGCACAGTAGATGGGACTCGCGATCCTCG 239

Db 101 GGGGCCACTTCTTGAGGATCCCTCCGGATGGCACAGTGGGCAAGGGACAGGAGCG 160

QY 240 ACCAGCACATTCAGCTGCAACTCTCGGCCGAAAGCGTTGGAGAGGTCTATATCAAGTCGA 299

Db 161 ACCAGCACATTCAGCTGCAACTCAGTCGGAAGCGTGGGGAGGTGTATATAAGAGTA 220

QY 300 CGGAGACTGGCAGTACCTTGCCATGGAACCCGATGGGCTTCTGTATGGCTCACAGAGCG 359

Db 221 CCGAGACTGGCAGTACTTGGCCATGGACACCGAGCGGCTTTTATACGGCTCACAGACAC 280

QY 360 CTAAAGGAATGCTGTGTTCTAGAAAGACTAGAGAAACCATTTACAAACAGTACATAT 419

Db 281 CAAATGAGGAATGTTGTTCTGGAAAGGCTGGAGGAGAACCATTTACAAACCTATATAT 340

QY 420 CGAAAAAATCATGCAGAGAAAGAACTGGTTTGTAGGCTTAAAAAAATGGTCTCTGTAAAGC 479

Db 341 CCAAGAGCATGCAGAGAGAAATGGTTGTTGGCTCAAGAGAAATGGGAGCTGCAAC 400

QY 480 GTGGACACCGACTCATATAGGCCAAAGGCTATCTTGTCTGCGACTACAGTAGAGCT 539

Db 401 GCGGTCTCGGACTCACTATGGCCAGAAAGCAATCTTGTCTCCCGCTGCCAGTCTCTT 460

RESULT 14

US-09-929-918-3

; Sequence 3, Application US/09929918
; Patent No. 6773899
; GENERAL INFORMATION:
; APPLICANT: Kordyum, Vitaliy A.
; APPLICANT: Chernykh, Svitlana I.
; APPLICANT: Slavchenko, Iryna Yu.

; APPLICANT: Vozianov, Oleksandr
; TITLE OF INVENTION: PHAGE-DEPENDENT SUPER PRODUCTION OF
; FILE REFERENCE: BIOLOGICALLY ACTIVE PROTEIN AND PEPTIDES
; CURRENT APPLICATION NUMBER: US/09/929,918
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 09/318,288
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-929-918-3

Query Match 45.1%; Score 284; DB 4; Length 468;

Best Local Similarity 79.0%; Pred. No. 3e-77;
Matches 338; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 120 ATATGTTTAACTTCGGCCCGGAATTACAAAAACCCAAAGTCTTCTTACTCGAGTAACG 179

Db 41 AGAAGTTTAACTTCGCTCCAGGGAATTACAGAAGCCCAAACTCTCTACTGTAGCAACG 100

QY 180 GAGGACATCTCCGGAATTCGCCAGATGGCACAGTAGATGGGACTCGCGATCCTCG 239

Db 101 GGGGCCACTTCTTGAGGATCCCTCCGGATGGCACAGTGGGCAAGGGACAGGAGCG 160

QY 240 ACCAGCACATTCAGCTGCAACTCTCGGCCGAAAGCGTTGGAGAGGTCTATATCAAGTCGA 299

Db 161 ACCAGCACATTCAGCTGCAACTCAGTCGGAAGCGTGGGGAGGTGTATATAAGAGTA 220

QY 300 CGGAGACTGGCAGTACCTTGCCATGGAACCCGATGGGCTTCTGTATGGCTCACAGAGCG 359

Db 221 CCGAGACTGGCAGTACTTGGCCATGGACACCGAGCGGCTTTTATACGGCTCACAGACAC 280

QY 360 CTAAAGGAATGCTGTGTTCTAGAAAGACTAGAGAAACCATTTACAAACAGTACATAT 419

Db 281 CAAATGAGGAATGTTGTTCTGGAAAGGCTGGAGGAGAACCATTTACAAACCTATATAT 340

QY 420 CGAAAAAATCATGCAGAGAAAGAACTGGTTTGTAGGCTTAAAAAAATGGTCTCTGTAAAGC 479

Db 341 CCAAGAGCATGCAGAGAGAAATGGTTGTTGGCTCAAGAGAAATGGGAGCTGCAAC 400

QY 480 GTGGACACCGACTCATATAGGCCAAAGGCTATCTTGTCTGCGACTACAGTAGAGCT 539

Db 401 GCGGTCTCGGACTCACTATGGCCAGAAAGCAATCTTGTCTCCCGCTGCCAGTCTCTT 460

RESULT 15

5437995-1

; Patent No. 5437995
; APPLICANT: ICHIMORI, YUZO; KONDO, KOICHI; IGARASHI, KOICHI;
; SENDO, MASAHARU
; TITLE OF INVENTION: MONOCLONAL ANIBODY AGAINST AN ACIDIC
; FGF PROTEIN AND HYBRIDOMA FOR ITS PRODUCTION
; NUMBER OF SEQUENCES: 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/26,257
; FILING DATE: 04-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 588,343
; FILING DATE: 26-SEP-1990
; SEQ ID NO:1:
; LENGTH: 450
5437995-1

Query Match 38.4%; Score 242; DB 6; Length 450;

Best Local Similarity 79.1%; Pred. No. 2.5e-64;

Matches 337; Conservative 0; Mismatches 85; Indels 4; Gaps 4;	
Qy	122 ATGTTTAACTTCCGCGCGGGAATTACAAAAACCCAGCTTCTTTACTGCGAGTAACGGA 181
Db	
Qy	14 ATGTTTAAATCTGCTCCCGGGAATTACAAAGAGCCCAAACTCCTCTACTGCGCAACCGG 73
Db	
Qy	182 GGACACTTCTCTGGAAATCTGCCAGATGGCAGATAGATGGGACTCGCGATCGCTCCGAC 241
Db	
Qy	74 GGCCACTTCTTGAGGATTTCTCCGGATGGACAGTGGATGGGACAAAGGA-CAGGACGAC 132
Db	
Qy	242 CAGCACATTCAAGTGCACCTCTGGCCGAAAGCGTTGGAGAGTCTATATCAAGTCGACG 301
Db	
Qy	133 CAGCACATTCAAGTGCACCTCTGGCCGAAAGCGTTGGAGAGTCTATATAAGAGTACC 192
Db	
Qy	302 GAGACTGGCCAGTACCTTGGCATGGACACCGATGGGCTTCTGTATGGCTCACAGAGCCT 361
Db	
Qy	193 GAGACTGGCCAGTA-CTTGGCAATGACACCGAGCGGCTTTTATACGGCTCACAGACACCA 251
Db	
Qy	362 AACGAAGAATGCTTGTCTTAGAAGACTAGAAAGAAACCATTTACAAACGTCACATATCG 421
Db	
Qy	252 AATGAGGAATGTTGTCTTGGAAAGCTGGAGGAGAACATTTACAACTATATATCC 311
Db	
Qy	422 AAAAAACATGCAGAGAACTGGTTTGTAGGCTTTAAAAAAATGGTTCTGTAAAGCGT 481
Db	
Qy	312 AAGAAGCATGCAGAGAAATTCCTTTGTGGCTCAAGAAGATGG-AGCTGCAAAACGC 370
Db	
Qy	482 GGACCAAGGACTCACTATGGCCAAAAGGCTATCTTGTCTGCCACTACCACTGAGCTCC 541
Db	
Qy	371 GGTCTCGGACTCACTAT-GCCAGAAAGCAATCTTGTCTCCCGCTGCCAGTCTCTTCT 429
Db	
Qy	542 GACTAA 547
Db	
Qy	430 GATTAA 435
Db	

Search completed: June 17, 2005, 02:31:24
Job time : 167 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 17, 2005, 00:13:55 ; Search time 2869 seconds
(without alignments)
8358.484 Million cell updates/sec

Title: US-10-649-480A-6
Perfect score: 630
Sequence: 1 gcgtagagatcgagatctc.....ctgagatcgggtgctaaca 630

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	285.4	45.3	534	1 AI590078	AI590078 tm58c01.x
2	285.4	45.3	821	4 BI598390	BI598390 603250094
3	285.4	45.3	1014	4 BM809005	BM809005 AGENCOURT
4	285.4	45.3	1098	5 BX444567	BX444567 BX444567
5	283	44.9	625	7 CV030767	CV030767 9975 Full1
6	275.2	43.7	1057	5 BQ067949	BQ067949 AGENCOURT
7	275	43.7	508	9 CG633840	CG633840 OST353987
8	275	43.7	635	7 CK624469	CK624469 m121e12.y
9	275	43.7	855	4 BI331990	BI331990 602984393
10	275	43.7	3404	3 AK035330	AK035330 Mus muscu
11	274.4	43.6	878	4 BI753845	BI753845 603027526
12	274.2	43.5	472	1 AI077609	AI077609 oy26d02.8
13	273.4	43.4	663	1 AI119291	AI119291 ue95c07.y
14	264.4	42.0	714	4 BG706412	BG706412 602669744
15	264	41.9	832	4 BI869731	BI869731 603393620
16	261.2	41.5	689	1 AI663400	AI663400 uk32d07.y
17	261	41.4	843	4 BI692283	BI692283 603342751
18	261	41.4	2206	3 EC027001	EC027001 Mus muscu
19	260.6	41.4	526	9 CG565930	CG565930 OST191133
20	260.6	41.4	631	2 BB627624	BB627624 BB627624
21	256.4	40.7	809	7 CO420661	CO420661 GGEZHC101
22	249.6	39.6	461	4 BF956865	BF956865 RCI-NN023
23	233.2	37.0	813	2 BF532970	BF532970 602073491
24	228.4	36.3	611	5 BU840197	BU840197 AGENCOURT

25	209.6	33.3	546	7	CR533323	CR533323 DKF2p459M
26	208.2	33.0	503	2	BF442355	BF442355 259038 WA
27	207.6	33.0	485	9	CG554707	CG554707 OST168594
28	203.4	32.3	750	5	BU627243	BU627243 UI-H-FGO-
29	203.2	32.3	543	1	AA261582	AA261582 mz87c09.r
30	203	32.2	395	6	CB773841	CB773841 AMGNNUC.S
31	194.8	30.9	529	9	CG629018	CG629018 OST340697
32	190.8	30.3	429	2	AW531286	AW531286 UI-R-C4-a
33	189	30.0	288	6	CB710781	CB710781 AMGNNUC.N
34	188.6	29.9	469	2	AW259195	AW259195 um89f09.Y
35	186.4	28.6	926	6	CD253719	CD253719 AGENCOURT
36	182.2	28.9	570	4	BM364189	BM364189 BS3000090
37	180	28.6	543	7	CR537204	CR537204 DKF2p459K
38	173.4	27.5	591	5	BU396096	BU396096 603801862
39	171	27.1	898	6	CD301410	CD301410 AGENCOURT
40	168.4	26.7	384	1	AA238828	AA238828 mx92h02.r
41	167.8	26.6	522	6	CD701495	CD701495 EST18019
42	164.4	26.1	458	1	AA594274	AA594274 nl90901.8
43	161.6	25.7	677	7	CV067690	CV067690 Le_mko.37
44	159.6	25.3	406	6	CB807695	CB807695 AMGNNUC.S
45	159.4	25.3	226	4	BI423446	BI423446 CM85 Deer

ALIGNMENTS

RESULT 1
AI590078/c
LOCUS AI590078 534 bp mRNA linear EST 21-APR-1999
DEFINITION tm58c01.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2162304 3', similar to gb:M13361 HEPARIN-BINDING GROWTH FACTOR PRECURSOR 1 (HUMAN);, mRNA sequence.
ACCESSION AI590078
VERSION AI590078.1 GI:4599126
KEYWORDS .EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 534)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGP), Tumor Gene Index
COMMENT Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www.bio.llnl.gov/bbrp/image/image.html
Insert length: 735 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 455.
Location/Qualifiers
1. 534
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2162304"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Brn25"
/note="Organ: brain; Vector: pTT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site 2: Eco RI; let strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTCAATCTGAAGTGGAGCGGCATAGTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pF713 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaído."

ORIGIN	Query Match	45.3%;	Score 285.4;	DB 1;	Length 534;
	Best Local Similarity	78.9%;	Pred. No. 6e-74;		
	Matches 340;	Conservative 0;	Mismatches 91;	Indels 0;	Gaps 0;
QY	120 ATATGTTTAACTTCGCGCCGGGAATTACAAAAACCCAAAGCTTCTTTACTGAGTAACG	179			
Db	464 AGAAGTTTAATCTGCGCTCCAGGGAAATTCAGAAGCCCAACTCCTCTACTGTAGCAACG	405			
QY	180 GAGGACACTTCCTCGGAATTTCTGCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCG	239			
Db	404 GGGGCCACTTCCTGAGGATCCTTCGGATGGCACAGTGGATGGGCAAGGGACNAGAGCG	345			
QY	240 ACCAGCACATTCAGCTGCAACTCTCGCGCGAAAGCGTTGGAGAGGCTCTATATCAAGTCGA	299			
Db	344 ACCAGCACATTCAGCTGCAGCTCAGTGCAGAAAGCGTGGGGAGGTGTATATAAGAGTA	285			
QY	300 CGGAGACTGGCCAGTACCTTGCATGGACACCGATGGGCTTCTGTATGGCTCACAGAGCG	359			
Db	284 CCAGAGCTGGCCAGTACTTGGCCATGGACACCGACGGGCTTTTATACGGCTCACAGACAC	225			
QY	360 CTAAAGAGAAATGCTTGTGTTCTAGAAAGACTAGAGAAACCATTTACACAGCTACATAT	419			
Db	224 CAAATGAGGAATGTTTGTTCCTGAAAGGCTGGAGGAGAACCATTTACACACCTTATATAT	165			
QY	420 CGAAAAACATCGAGAGAAGAACTGGTTGTAGGCTTTAAAAAATGTTTCTGTGAAGC	479			
Db	164 CCAAGAGCATTCAGAGAGAAGAAATGGTTGTGTGGCTCAAGAGAAATGGGAGCTGCAAC	105			
QY	480 GTGGACACCGGACTCACTATGCGCCAAAGGCTATCTTGTTCCTGCCACTACCAAGTGAGCT	539			
Db	104 GCGGTCTCGGACTCACTATGGCCAGAAAGCAATCTTGTGTTCTCCCCCTGCCAGTCTCTT	45			
QY	540 CCGACTAAAGGA 550				
Db	44 CTGATTAAAGA 34				

RESULT 2
BI598390
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

BI598390 821 bp mRNA linear EST 07-SEP-2001
603250094F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5302030 5',
mRNA sequence.
BI598390
BI598390.1 GI:15491329
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 821)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11764 row: k column: 23
High quality sequence stop: 777.
Location/Qualifiers
1. .821

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5302030"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_96"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site: BamHI; Site 2: SalI-XhoI
(gtcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NHGRI/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

ORIGIN	Query Match	45.3%;	Score 285.4;	DB 4;	Length 821;
	Best Local Similarity	78.9%;	Pred. No. 6.7e-74;	Mismatches 91;	Indels 0; Gaps 0;
	Matches 340;	Conservative 0;			
QY	120 ATATGTTTAACTTCGCGCCGGGAATTACAAAAACCCAAAGCTTCTTTACTCGAGTAACG	179			
DB					
QY	180 GAGGACACTTCCTCGGAATTTGCCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCG	239			
DB					
QY	240 ACCAGCACATTCAGCTGCAACTCTCGGCGCAAGCGTTGGAGAGCTCTATATCAAGTCGA	299			
DB					
QY	300 CGGAGACTGGCCAGTACCTTGCATGGACACCGATGGGCTTCTGTATGGCTCACAGAGCG	359			
DB					
QY	360 CTAAAGAGAAATGCTTGTGTTCTAGAAAGACTAGAGAAACCATTTACACAGGTACATAT	419			
DB					
QY	420 CGAAAAACATCGACAGAGAACTGGTTGTAGGCTTTAAAAAATGTTCTCTTAAGC	479			
DB					
QY	480 GTGGACACCGACTCACTATGCGCAAAAGGCTATCTTGTTCCTGCGCACTACCAAGTGAGCT	539			
DB					
QY	540 CCGACTAAAGGA 550				
DB					
DB	610 CTGATTAAAGA 620				
RESULT 3	BM809005				
LOCUS	AGENCOURT 6617747 NIH_MGC_124 Homo sapiens	1014 bp	mRNA	linear	EST 05-MAR-2002
DEFINITION	5', mRNA Sequence.				
ACCESSION	BM809005				
VERSION	BM809005.1	GI:19125828			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE	1 (bases 1 to 1014)				
JOURNAL	NIH-MGC http://mgs.nci.nih.gov/				
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)				
	Unpublished (1999)				
	Contact: Robert Strausberg, Ph.D.				

RESULT 3
BM809005
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

BM809005 1014 bp mRNA linear EST 05-MAR-2002
AGENCOURT 6617747 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:573445
5', mRNA sequence.
BM809005
BM809005.1 GI:19125828
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1014)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Cloning Distribution: Agencourt Bioscience Corporation
Cloning Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12739 row: m column: 06
High quality sequence stop: 637.
Location/Qualifiers
1. .1014
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5734445"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH MGC 124"
/notes="Organ: brain; Vector: pCMV-SPORT6; Site 1: EcoRV (destroyed); Site 2: NotI; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."
45.3%; Score 285.4; DB 4; Length 1014;
Best Local Similarity 78.9%; Pred. No. 7.1e-74;
Matches 340; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

FEATURES source

ORIGIN

Query Match 45.3%; Score 285.4; DB 4; Length 1014;
Best Local Similarity 78.9%; Pred. No. 7.1e-74;
Matches 340; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 120 ATATGTTTAACTTCGCGCGGAATTACAAAACCCAAAGCTTCTTACTGCAGTAACG 179
DB 223 AGAAGTTTAACTTCGCGCGGAATTACAAAACCCAAAGCTTCTTACTGTAGCAACG 282

QY 180 GAGGACACTTCGCGGAATTCTCCAGATGGCACAGTAGATGGGACTCGCGTCCG 239
DB 283 GGGGCCACTTCCTGAGGATCCITCCGATGGCACAGTAGATGGGACAGGAGCG 342

QY 240 ACCAGACACTTCAGCTGCAGCTCAGTGGGAAAGCGTTGGAGAGGTCTATATCAAGTCGA 299
DB 343 ACCAGACACTTCAGCTGCAGCTCAGTGGGAAAGCGTTGGAGAGGTCTATATAAGAGTA 402

QY 300 CGGAGACTGGCCAGTACCTTGGCATGGACACCGATGGGCTTCTGTATGGCTCACAGCG 359
DB 403 CGGAGACTGGCCAGTACCTTGGCATGGACACCGATGGGCTTCTGTATGGCTCACAGCG 462

QY 360 CTAAACGAGATGCTTGTCTTCTAGAGACTAGAGAAACCATTAACAACCGTACATAT 419
DB 463 CAAATGAGGAATGTTTGTCTTCTGGAAGGCTGGAGGAGAACCATTAACAACCGTACATAT 522

QY 420 CGAAAAACATGACAGAGAACTGGTTTGTAGGCTTTAAAAAATGGTTCTCTGTAAGC 479
DB 523 CCAGAGAGCATGACAGAGAAATGGTTTGTGGCTTCAAGAGATGGGAGCTGCAAC 582

QY 480 GTGGACACCGACTCACTATGGCCAAAGGCTATTTGTTCTTCCGCCACTACCGATGAGCT 539
DB 583 CGGCTCTCGGACTCACTATGGCCAAAGGCTATTTGTTCTTCCGCCACTACCGATGAGCT 642

QY 540 CCGACTAAGA 550
DB 643 CTGATTAAGA 653

RESULT 4
BX444567
LOCUS
DEFINITION BX444567 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
CSODN003YP16 5-PRIME, mRNA sequence.
ACCESSION BX444567
VERSION BX444567.2 GI:47009158

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1098)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 15, 2003 this sequence version replaced gi:30780253.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremlieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 3201.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODN003DH08QP1&c=3201.r.

FEATURES
source

Location/Qualifiers
1. .1098
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODN003YP16"
/tissue_type="ADULT BRAIN"
/dev_stage="adult"
/clone_lib="Homo sapiens ADULT BRAIN"
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN

Query Match 45.3%; Score 285.4; DB 5; Length 1098;
Best Local Similarity 78.9%; Pred. No. 7.2e-74;
Matches 340; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 120 ATATGTTTAACTTCGCGCGGAATTACAAAACCCAAAGCTTCTTACTGCAGTAACG 179
DB 151 AGAAGTTTAACTTCGCGCGGAATTACAAAACCCAAAGCTTCTTACTGTAGCAACG 210

QY 180 GAGGACACTTCGCGGAATTCTCCAGATGGCACAGTAGATGGGACTCGCGTCCG 239
DB 211 GGGGCCACTTCCTGAGGATCCITCCGATGGCACAGTAGATGGGACAGGAGCG 270

QY 240 ACCAGACACTTCAGCTGCAGCTCAGTGGGAAAGCGTTGGAGAGGTCTATATCAAGTCGA 299
DB 271 ACCAGACACTTCAGCTGCAGCTCAGTGGGAAAGCGTTGGAGAGGTCTATATAAGAGTA 330

QY 300 CGGAGACTGGCCAGTACCTTGGCATGGACACCGATGGGCTTCTGTATGGCTCACAGCG 359
DB 331 CGGAGACTGGCCAGTACCTTGGCATGGACACCGATGGGCTTCTGTATGGCTCACAGCG 390

QY 360 CTAAACGAGATGCTTGTCTTCTAGAAAGACTAGAGAAACCATTAACAACCGTACATAT 419
DB 391 CAAATGAGGAATGTTTGTCTTCTGGAAGGCTGGAGGAGAACCATTAACAACCGTACATAT 450

QY 420 CGAAAAACATGACAGAGAACTGGTTTGTAGGCTTTAAAAAATGGTTCTCTGTAAGC 479
DB 451 CCAGAGAGCATGACAGAGAAATGGTTTGTGGCTTCAAGAGATGGGAGCTGCAAC 510

QY 480 GTGGACACCGACTCACTATGGCCAAAGGCTATTTGTTCTTCCGCCACTACCGATGAGCT 539
DB 511 CGGCTCTCGGACTCACTATGGCCAAAGGCTATTTGTTCTTCCGCCACTACCGATGAGCT 570

QY 540 CCGACTAAGA 550
DB 571 CTGATTAAGA 581

QY 120 ATATGTTTAACTTCGCGCCGGGAATTACAAAAACCCCAAGCTCTTTTACTGCACTAACG 179
DB 181 AGAAGTTTAACTTCGCTCCAGGGAATTACAGAGCCCAAACTCTCTACTGTAGCAACG 240
QY 180 GAGGACACTTCCTCGGAAATTCGCCAGATGGCACAGTAGATGGGACTCGCGATCGCTCG 239
DB 241 GGGGCCACTTCCTGAGGATCCTTCGGATGGCACAGTAGTGGGCAAGGGACAGGAGCG 300
QY 240 ACCAGCACATTCAGTGGCAACTCTCGGCCGAAGCGTTGGAGAGGTCTATATCAAGTCGA 299
DB 301 ACCAGCACATTCAGTGGCAACTCTCGGCCGAAGCGTTGGAGAGGTCTATATCAAGTCGA 360
QY 300 CGGAGACTCGGAGTACCTTCGATGACGACACCGATGGGCTCTGTATGCTCACAGACGC 359
DB 361 CGGAGACTCGGAGTACCTTCGATGACGACACCGATGGGCTCTGTATGCTCACAGACGC 420
QY 360 CTAACGAAGAATGCTTGTCTAGAAAGACTAGAAAGAAACCATTAACAACGTCATAT 419
DB 421 CAAATGAGGAATGCTTGTCTAGAAAGACTAGAAAGAAACCATTAACAACGTCATAT 480
QY 420 CGAAAAAATGAGGAGAACTGTTGTAGGCTTAAAAAATGTTTCTGTAAAGC 479
DB 481 CCAAGAAGCATGAGAGAAATGTTGTGTCCTCAAGAAGAAATGGGAGCTGCMAAC 540
QY 480 GTGACACGAGTCACTATGGCCAAAGGCTATCTTGTCTGCGCAC 527
DB 541 GCGGTCTCGGACTACTATGGCCAGAAAGCAATCTTGTCTTCCCCC 588

RESULT 7
CG633840 508 bp mRNA linear GSS 02-OCT-2003
LOCUS OST353987 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST353987,
DEFINITION mRNA sequence.
ACCESSION CG633840.1 GI:37457689
VERSION CG633840
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 508)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Zambrowicz,B.P., Ahuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparks,M.J., Van Slightenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.

TITLE Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT Contact: Zambrowicz BP
OnniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.

FEATURES
source
1. 508
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST353987"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN
Query Match 43.7%; Score 275; DB 9; Length 508;
Best Local Similarity 77.8%; Pred. No. 7.7e-71;

Matches 332; Conservative 0; Mismatches 95; Indels 0; Gaps 0;
QY 120 ATATGTTTAACTTCGCGCCGGGAATTACAAAAACCCCAAGCTCTTTTACTGCACTAACG 179
DB 79 AGAGTTTAACTTCGCTCCAGGGAATTACAGAGCCCAAACTCTCTACTGTAGCAACG 138
QY 180 GAGGACACTTCCTCGGAAATTCGCCAGATGGCACAGTAGATGGGACTCGCGATCGCTCG 239
DB 139 GGGGCCACTTCCTGAGGATCCTTCGATGACGACCGTGGATGGGCAAGGGACAGGAGCG 198
QY 240 ACCAGCACATTCAGTGGCAACTCTCGGCCGAAGCGTTGGAGAGGTCTATATCAAGTCGA 299
DB 199 ACCAGCACATTCAGTGGCAACTCTCGGCCGAAGCGTTGGAGAGGTCTATATCAAGTCGA 258
QY 300 CGGAGACTCGGAGTACCTTCGATGACGACACCGATGGGCTCTGTATGCTCACAGACGC 359
DB 259 CGGAGACTCGGAGTACCTTCGATGACGACACCGATGGGCTCTGTATGCTCACAGACGC 318
QY 360 CTAACGAAGAATGCTTGTCTAGAAAGACTAGAAAGAAACCATTAACAACGTCATAT 419
DB 319 CAAATGAGGAATGCTTGTCTAGAAAGACTAGAAAGAAACCATTAACAACGTCATAT 378
QY 420 CGAAAAAATGAGGAGAACTGTTGTAGGCTTAAAAAATGTTTCTGTAAAGC 479
DB 379 CCAAGAAGCATGAGAGAAATGTTGTGTCCTCAAGAAGAAATGGGAGCTGTAAAGC 438
QY 480 GTGACACGAGTCACTATGGCCAAAGGCTATCTTGTCTGCGCAC 527
DB 439 GCGGTCTCGGACTACTATGGCCAGAAAGCAATCTTGTCTTCCCCC 498
QY 540 CCGGACTA 546
DB 499 CTGACTA 505

RESULT 8
CK624469 635 bp mRNA linear EST 26-JAN-2004
LOCUS mi21e12.Y1 Mouse RPE/choroid, unamplified: mi/mj Mus musculus cDNA
DEFINITION clone mi21e12 5', mRNA sequence.
ACCESSION CK624469
VERSION CK624469.1 GI:41345355
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 635)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Ida,H., Boylan,S., Weigel,A., Smit-McBride,Z., Chao,A., Gao,J.,
Buchhoff,P., Wistow,G. and Hjelmeland,L.

TITLE Expressed sequence tag analysis of mouse RPE/choroid
JOURNAL Unpublished (2004)
COMMENT Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 21 row: e column: 12
Seq primer: M13RPI reverse primer (ABI).

FEATURES
source
1. 635
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL6J"
/db_xref="taxon:10090"
/clone="mi21e12"
/sex="Male"
/tissue_type="RPE/choroid"
/dev_stage="Adult"
/lab_host="EMDH108"
/clone_lib="Mouse RPE/choroid, unamplified: mi/mj"

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLML1495 row: d column: 08
High quality sequence stop: 703.
Location/Qualifiers
1. .878
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5197783"
/lab_host="DH10B"
/clone_lib="NIH_MGC_114"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."

FEATURES
source

ORIGIN

Query Match 43.6%; Score 274.4; DB 4; Length 878;
Best Local Similarity 78.7%; Pred. No. 1.3e-70;
Matches 340; Conservative 0; Mismatches 91; Indels 1; Gaps 1;
QY 120 ATATGTTTAACTTCGCGCGGGAATTACAAAACCC--AAGCTTCTTACTGCGAGTAAC 178
DB 157 AGAAGTTTAACTTCGCGCGGGAATTACAAAACCC--AAGCTTCTTACTGCGAGTAAC 216
QY 179 GAGAGACACTTCTGCGAATTCGCCAGATGGCAGATAGATGGGACTCGCGACTCGCTCC 238
DB 217 GGGGGCCACTTCTGAGGATCTTCGGATGGCAGATGGGAGGACAGGAGGAGC 276
QY 239 GACAGACATTCAGCTGCAACTCTGCGCGGAAAGCGTTGGAGAGGTCTATATCAAGTCG 298
DB 277 GACAGACATTCAGCTGCAACTCTGCGCGGAAAGCGTTGGAGAGGTCTATATAAGAGT 336
QY 299 ACGGAGCTGGCGGAGTCTGCGGAGGACGAGTGGCTTCTGTATGGCTCACAGG 358
DB 337 ACCGAGCTGGCGGAGTCTGCGGAGGACGAGTGGCTTCTGTATGGCTCACAGG 396
QY 359 CCTAACGAGAAATGCTTGTGTTCTAGAAAGACTAGAGAAACCATTTACAAACGTACATA 418
DB 397 CCATATGAGGATGTTGTTCTCGGAAAGCTGGAGGAGAACATTTACAAACCTATATA 456
QY 419 TCGAAAAAATGCGAGAGAAAGTGGTTGTAGGCTTTAAAAAATGGTTCTGTGAAG 478
DB 457 TCCAAAGACGATGAGAGAAAGTGGTTGTAGGCTTCAAGAAGAAATGGGAGCTGCAA 516
QY 479 CGTGGACACGAGTCACTATGGCCAAAGGCTATCTGTTCTGCCACTACCACTGAGC 538
DB 517 CGCGTCTCGGAGTCACTATGGCCAAAGGCAATCTTGTATCTCCCCCTGCCAGTCTCT 576
QY 539 TCCGACTAAGGA 550
DB 577 TCTGATTAAGA 588

RESULT 12
AI077609/c
LOCUS
DEFINITION
oy26d02.al Soares senescent fibroblasts NbHSP Homo sapiens CDNA
clone IMAGE:1666947 3' similar to gb:MI3361 HEPARIN-BINDING GROWTH
FACTOR PRECURSOR 1 (HUMAN) ; mRNA sequence.
AI077609
ACCESSION
VERSION
AI077609.1 GI:3412017
KEYWORDS
EST.

SOURCE
ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 472)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

REFERENCE
AUTHORS
TITLE

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 649 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. .472
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1666947"
/tissue_type="senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares senescent fibroblasts_NbHSP"
/note="vector: pT7T3p (pharmacia) with a modified
polylinker V.TYPE: phagemid; Site 1: Not I; Site 2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo (dtr)
primer [5',
TGTTACCAATCTGAAGTGGGAGCGCGCATTTTTTTTTTTTTTTT 3',
double-stranded cDNA was size selected, ligated to Eco RI
adapters (pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo."

FEATURES
source

Query Match 43.5%; Score 274.2; DB 1; Length 472;
Best Local Similarity 77.3%; Pred. No. 1.3e-70;
Matches 333; Conservative 0; Mismatches 98; Indels 0; Gaps 0;
QY 120 ATATGTTTAACTTCGCGCGGGAATTACAAAACCCAGCTTCTTTACTGCGAGTAACG 179
DB 461 AGAAGTTTAACTTCGCGCGGGAATTACAAAACCCAGCTTCTTTACTGTAACGACG 402
QY 180 GAGGACACTTCTCGCAATTCGCCAGATGGCAGATAGATGGGACTCGCGATCGCTCCG 239
DB 401 GGGCTCACTTCTGAGCGATCTTCGGATGGCAGTGGATGGAAACAGGACAGGAGCG 342
QY 240 ACCAGCACATTCAGCTGCAACTCTCGGCGGAAAGCGTTGGAGAGGTCTATATCAAGTCGA 299
DB 341 ACCAGCACATTCAGCTGCAACTCTCGGCGGAAAGCGTTGGAGAGGTCTATATAAGAGTA 282
QY 300 CGGAGACTGGCCAGTACCTTGCCTATGGACACCGATGGGCTTCTGTATGGCTCACAGGCG 359
DB 281 CCGAGACTTGGCAGTACTTGGCCATGGACACCGACGGGCTTTTATACGGCTCACAGAC 222
QY 360 CTAACGAGAAATGCTTGTCTAGAAAGACTAGAGAAACCATTTACAAACGTCATATAT 419
DB 221 CAATGAGGAATTTTGTCTCGGAGGCGTGGAGGAGNACCATTTACACACCTATATAT 162
QY 420 CGAAAAAATGCGAGAGAAACTGGTTTGTAGGCTTTAAAAAATGGTTCTCTGTGAAGC 479
DB 161 CCAAGAAGCATGCGAGAGAAATTTGGTTTGTGGCTTCAAGAAGAAATGGGAGCTGCAAC 102
QY 480 GTGACACACGAGTCACTATGGCCAAAGGATCTTGTTCCTGCCACTACCACTGAGCT 539
DB 101 CGGCTCTCGGACTCACTATGGCCAAAGGCAATCTTGTTCCTCCCTGCCCTGCTCTCT 42
QY 540 CCGACTAAGGA 550

ORIGIN

```

Db
41 CTGATTAAAGA 31

RESULT 13
AII19291
LOCUS
DEFINITION
    ue95c07.y1 Sugano mouse embryo mewa Mus musculus cDNA clone
    IMAGE:1498860 5' similar to gb:M13361 HEPARIN-BINDING GROWTH FACTOR
    PRECURSOR 1 (HUMAN);, mRNA sequence.
ACCESSION
    AII19291
VERSION
    AII19291.1 GI:3519615
KEYWORDS
    EST.
SOURCE
    Mus musculus (house mouse)
ORGANISM
    Mus musculus
REFERENCE
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
    1 (bases 1 to 663)
AUTHORS
    Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
    Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
    Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
    Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
    Waterston,R.
TITLE
    The WashU-HHMI Mouse EST Project
JOURNAL
    Unpublished (1996)
COMMENT
    Contact: Marra M/Mouse EST Project
    WashU-HHMI Mouse EST Project
    Washington University School of Medicine
    4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
    Tel: 314 286 1800
    Fax: 314 286 1810
    Email: mouseest@wustl.edu
    This clone is available royalty-free through LLNL; contact the
    IMAGE Consortium (info@image.llnl.gov) for further information.
    MGI:936464
    Seq primer: custom primer used
    High quality sequence stop: 527.

FEATURES
    source
    1..663
    /organism="Mus musculus"
    /mol_type="mRNA"
    /strain="C57BL"
    /db_xref="taxon:10090"
    /clone="IMAGE:1498860"
    /dev_stage="embryo, 14 dpc"
    /lab_host="DH10B"
    /clone_lib="Sugano mouse embryo mewa"
    /notes="Vector: pME18S-FL3; Site 1: DraIII (CACTGTGTG);
    Site 2: DraIII (CACCATGTG); 1st strand cDNA was primed
    with an oligo(dT) primer [ATGTGGCCTTTTCTTTTCTTTT];
    double-stranded cDNA was ligated to a DraIII adaptor
    [TGTGGCTTACTGG], digested and cloned into distinct DraIII
    sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
    CACCATGTG). XhoI should be used to isolate the cDNA
    insert. Size selection was performed to exclude fragments
    <1.5kb. Library constructed by Dr. Sumio Sugano
    (University of Tokyo Institute of Medical Science).
    Custom primers for sequencing: 5' end primer
    CTTCCTGCTCTAAAGCTGGC and 3' end primer
    CGACCTGCAGCTCGAGCACA."

ORIGIN
    Query Match 43.4%; Score 273.4; DB 1; Length 663;
    Best Local Similarity 77.5%; Pred. No. 2.5e-70;
    Matches 331; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

Qy 120 ATATGTTTAACTTCGCCCGGGGAATTACAAAACCAAGCTCTTTTACTGCAGTAACG 179
Db 216 AGAGTTCAACCTCGCTCTTAGGAACACTACAAAAGCCAACTGCTCTACTGCAGCAACG 275
Qy 180 GAGGACACTTCTCGCAATTTCTGCAGATGCACAGTAGATGGAGCTTCGCGACTCGCTCCG 239
Db 276 GGGGCCACTTCTTGAGGATCTCTCTGATGGCACCCTGGATGGGACAAAGGACAGGAGCG 335

```

```

Qy 240 ACCAGCACATTTCAGCTGCAACTCTCGCGCGAAACGTTGGAGAGGTCTATATCAAGTCGA 299
Db 336 ACCAGCACATTTCAGCTGCAACTCTCGCGCGAAAGTCGGGGCGAAGTGTATATAAAGGCTA 395
Qy 300 CGGAGACTGGCCAGTACTTCCCATGGACACCGATGGGCTTCTGTATGGCTCACAGACGC 359
Db 396 CGGAGACCGGCGAGTACTTGGCCATGGACACCGAAGGCTTTTATACGGCTCGCAGACAC 455
Qy 360 CTAACGAGAATGCTGTGTTCTAGAAAGACTAGAAAGAAACCATTTACAAACGTCACATAT 419
Db 456 CAAATGAGGAATGCTGCTCTCTGGAAGGCTGGGAAGAAACCATTTATACACTTACACCT 515
Qy 420 CGAAAAAATCATCGAGAGAACTGGTTTGTAGCCCTTAAAAAAATGGTTCCTGTAAAGC 479
Db 516 CCAAGAACATCGCGAGAAAGAACTGGTTTGTGGGCTCAAGAAGAAACGGGAGCTGTAAAGC 575
Qy 480 GTGAGACACGAGTCACTATGCGCAAGGCTATCTTGTCTCCCTACCTACCACTGAGCTG 539
Db 576 GCGGTCTCTCGACTCACTATGCGCAGAAAGCAATCTTGTCTGCCCTCCCGGTGCTT 635
Qy 540 CCGACTA 546
Db 636 CTGACTA 642

```

```

RESULT 14
BG706412
LOCUS
DEFINITION
    602669744F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4792378 5',
    mRNA sequence.
ACCESSION
    BG706412
VERSION
    BG706412.1 GI:13981735
KEYWORDS
    EST.
SOURCE
    Homo sapiens (human)
ORGANISM
    Homo sapiens
REFERENCE
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
    1 (bases 1 to 714)
    NIH-MGC http://mgi.nci.nih.gov/
    National Institutes of Health, Mammalian Gene Collection (MGC)
    Unpublished (1999)
    Contact: Robert Strausberg, Ph.D.
    Email: cgabbs@mai.nih.gov
    Tissue procurement: Miklos Palkovits, M.D., Ph.D.
    cDNA library preparation: Michael J. Brownstein (NHGRI), Shiraki
    Toshiyuki and Piero Carninci (RIKEN)
    cDNA library arrayed by: The I.M.A.G.E. Consortium (LLNL)
    DNA Sequencing by: Incyte Genomics, Inc.
    Clone distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/LLNL at:
    http://image.llnl.gov
    Plate: LLN10870 row: h column: 11
    High quality sequence stop: 710.

```

FEATURES

```

    source
    1..714
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:4792378"
    /tissue_type="hypothalamus"
    /lab_host="DH10B"
    /clone_lib="NIH MGC 96"
    /notes="Organ: brain; Vector: pBluescriptR (modified
    pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
    (gtcgag); Oligo-dT primed using primer
    5'-TTTTTTTTTTTNN-3', size-selected for average
    insert size 2.3 kb and normalized to ROT 5. This is a
    primary library enriched for full-length clones and
    constructed using the Cap-trapper method (Carninci, in
    preparation). Library constructed by M. Brownstein
    (NIH/NHGRI, National Institutes of Health). Note: this is
    a NIH_MGC Library."

```

ORIGIN

